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<b>(54) Title:</b> PROCESSES FOR PRODUCING POLYHYDROXYBUTYRATE AND RELATED POLYHYDROXYALKANOATES IN THE PLASTIDS OF HIGHER PLANTS			
<b>(57) Abstract</b> <p>The present invention relates to a process for producing poly-D-(-)-3-hydroxybutyric acid (PHB) and related polyhydroxyalkanoates (PHA) in the plastids of plants. The production of PHB is accomplished by genetically transforming plants with modified genes from microorganisms. The genes encode the enzymes required to synthesize PHB from acetyl-CoA or related metabolites and are fused with additional plant sequences for targeting the enzymes to the plastid.</p>			

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**PROCESSES FOR PRODUCING POLYHYDROXYBUTYRATE AND  
RELATED POLYHYDROXYALKANOATES IN THE PLASTIDS  
OF HIGHER PLANTS**

Cross-Reference to Related Application

This application is a continuation-in-part of U.S. application Serial No. 08/108,193, filed August 17, 1993, which is a continuation-in-part of 07/732,243, filed July 19, 1991.

Government Rights

The invention described herein was made in the course of work under grant number DE-AC02-76ERO-1338 from the U.S. Department of Energy and No. DMB 9014037 from the National Science Foundation. The U.S. Government has certain rights under this invention.

BACKGROUND OF THE INVENTION

(1) Field of the Invention

This patent concerns inventions which improve the production of a class of material called polyhydroxyalkanoates (PHA) in higher plants. PHA is a group of bacterial polymeric material composed of linear polyesters of hydroxy acids and has thermoplastic properties. A low level production of PHA has previously been demonstrated in *Arabidopsis thaliana* transformed with the bacterial genes involved in PHA synthesis as described in Serial No. 07/732,243, filed July 19, 1991. In order to produce large amounts of PHAs in higher plants, the enzymes for PHA production have to be located in a subcellular compartment possessing a high level of precursor for PHA synthesis which is the plastid. The three genes of *Alcaligenes eutrophus* involved in synthesis of PHA from acetyl-CoA were modified to target the corresponding enzymes to the plastid of *Arabidopsis* plant cells as a specific example of the present invention.

(2) Description of Related Art

Polyhydroxyalkanoates (PHA), polyesters of 3-

nydroxyacids, are produced as carbon storage reserves by a large variety of bacteria (Anderson, A. J. and Dawes, E. A., Microbiol. Rev. 54: 450-472, 1990). Poly-D-(-)-3-hydroxybutyrate (PHB), the most widespread and thoroughly characterized PHA, is a biodegradable and biocompatible thermoplastic.

Research on PHA production has been mainly concentrated on *Alcaligenes eutrophus* which produces short chain PHAs ( $C_3$  to  $C_5$  units). In *A. eutrophus*, PHB is synthesized from acetyl-CoA by the sequential action of three enzymes (Figure 1) (Steinbüchel, A. and Schlegel, H. G., Mol. Microbiol. 5: 535-542, 1991). The first enzyme of the pathway, 3-ketothiolase (E.C. 2.3.1.9), catalyzes the reversible condensation of two acetyl-CoA moieties to form acetoacetyl-CoA. Acetoacetyl-CoA reductase (E.C. 1.1.1.36) subsequently reduces acetoacetyl-CoA to D-(-)-3-hydroxybutyryl-CoA, which is then polymerized by the action of PHB synthase to form PHB. PHB is produced as a polymer of  $10^5$ - $10^6$  monomer units which is accumulated in granules of 0.2 to 0.5  $\mu m$  in diameter, each granule containing approximately 1000 polymer chains (Anderson, A. J. and Dawes, E. A., Microbiol. Rev. 54: 450-472, 1990). When grown in medium containing glucose, *A. eutrophus* typically accumulates PHB up to 80% dry weight. The genes encoding the three *phb* biosynthetic enzymes described above have been cloned from *A. eutrophus* (Peoples, O. P. and Sinskey, A. J., J. Biol. Chem. 264: 15293-15297, 1989 and J. Biol. Chem. 264: 15298-15303, 1989; Slater, S. C., Voige W. H. and Dennis, D. E., J. Bacteriol. 170: 4431-4436, 1988, Schubert, P., Steinbüchel, A. and Schlegel, H. G., J. Bacteriol. 170: 5837-5847, 1988).

In addition to PHB homopolymer, *A. eutrophus* and other bacterial species can produce polymers containing various ratios of a number of different  $C_3$  to  $C_5$  monomers. The nature and proportion of these monomers is influenced by the carbon source supplied in the

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growth media. For example, when propionic acid or pentanoic acid is supplied to the fermentation feedstock, a random copolymer containing both 3-hydroxybutyrate (3HB) and 3-hydroxyvalerate (3HV) monomers is produced with a maximum of 43 mol% to 90 mol% of 3HV unit, respectively (Anderson, A. J. and Dawes, E. A., Microbiol. Rev. 54: 450-472, 1990). These PHA copolymers are synthesized by the same PHB synthase using the coenzyme A thioester derivatives of the C<sub>3</sub> to C<sub>5</sub> organic acids.

In addition to PHB and copolymers containing PHB, there is another general class of PHAs containing monomer units ranging between C<sub>6</sub> and C<sub>12</sub>. *Pseudomonas oleovorans* is the prototypical bacterium synthesizing PHAs containing medium-chain (D)-3-hydroxyacids when n-alkanes or n-alkanoic acids are provided in the growth media. The best studied of these PHAs is polyhydroxyoctanoate, which is accumulated when *P. oleovorans* is grown in a medium containing octanoate (Huisman, G. W., de Leeuw, O., Eggink, G., and Witholt, B. Appl. Environ. Microbiol. 54: 2924, 1988). Furthermore, unique polymers possessing unsaturated or branched chain monomers, as well as possessing chloride or fluoride side groups, can be obtained by manipulation of the fermentation feedstock (Doi, Y. (ed), In: Microbial polyesters, Chpt. 3, VCH Publisher, New York (1990).

PHB is a stiff and relatively brittle thermoplastic (Doi, Y. (ed) In: Microbial Polyesters, Chpt. 6, VCH Publishers, New York, 1990; Holmes, P. A. In: Developments in crystalline polymers-2. Basset, D. C. (ed), 1-65, 1988). Incorporation of 3HV monomers into the polymer leads to a decrease in crystallinity and melting point compared to PHB, resulting in a decrease in stiffness and an increase in toughness of the polymer, making P(3HB-co-3HV) and other related copolymers more suitable for many commercial

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applications. It is also possible to blend various polymers and plasticizers to PHB in order to improve its physical characteristics (Holmes, P. A. In: Developments in crystalline polymers-2. Basset, D. C. (ed), 1-65, 1988). PHB has good UV resistance but generally poor resistance to acids and bases as well as organic solvents. PHB possesses good oxygen impermeability and is resistant to hydrolytic degradation in moist air. These properties makes PHB attractive as a source of plastic for a wide range of commodity products, such as household containers, bags and wrapping films. In contrast to PHB, long-chain PHAs are elastomers with a melting point ranging from 40-60 °C (Gross, R. A., De Mello, C., Lenz, R. W., Brandl, H. and Fuller R. C. , Macromolecules 22: 1106, 1989). The physical properties of these PHAs have yet to be fully characterized.

PHB and related copolymers are readily degraded in soil, sludge and sea water. For example, in soil at 30°C, films of P(3HB-co-4HB) copolymer and PHB homopolymer are decomposed in two and ten weeks, respectively (Doi, Y. (ed) In: Microbial Polyesters, Chpt.1, VCH Publishers, New York, 1990). A number of bacteria and fungi were shown to be able to actively degrade these polymers (Dawes, E. A. and Senior, P. J., Adv. Microb. Physiol. 10: 135-266 (1973). Extracellular PHB depolymerases and hydrolases have been isolated from several bacteria, including *Alcaligenes feacalis*. PHB can thus be degraded to monomeric 3HB units which can be used as a source of carbon for bacterial and fungal growth. Furthermore, PHB is very biocompatible, making it potentially attractive for medical applications such as suture filaments and drug carriers (Koosha, F., Muller, R. H. and Davis, S. S. In: Critical reviews in therapeutic drug carrier system, 6: 117-129, 1989). Degradation of PHB produces D-3-hydroxybutyric acid, a metabolite normally present in blood. The biodegradation of PHB is an important aspect of its

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usefulness as a plastic for commodity disposable products, as well as for specialized uses such as in agricultural mulches or medical implants.

5 P(3HB-co-3HV) copolymer synthesized by *A. eutrophus* is produced industrially by Imperial Chemical Industries and marketed under the trademark BIOPOL. Estimated cost based on a production of 500000 kg of polymer a year is approximately \$15 per kg, in contrast to approximately \$1 per kg for petroleum-derived commodity plastics such as polypropylene (Poole, R, Science 245: 1187-1189, 1989). Two major contributors to the cost of production are the carbon source added to the feedstock (eg sucrose, glucose, propionate) and harvesting of the polymer from the bacteria. A number of strategies are being explored to reduce the production cost (Poirier, Y., Dennis, D. E., Nawrath, C. and Somerville, C. Adv. Mater. 5: 30-36, 1993). For example, some bacteria are able to produce PHB when grown on cheap unrefined sugar sources such as molasses and corn syrup. Some strains of *Pseudomonas* and *Rhodococcus* are able to produce a number of PHA copolymers when grown on glucose, thus avoiding the addition of expensive substrates, like propionate, normally required for copolymer production. Genetic engineering of bacteria, including the use of *E. coli* synthesizing PHB, is also expected to have an impact on production cost of PHB. However, despite these potential improvements, it is generally agreed that due to the inherent costs associated with bacterial fermentation and downstream processing, the cost of PHA produced by bacteria will probably not be lower than approximately \$3-5 per kg. It is unlikely that it will ever be possible to produce bacterial biomass at a cost comparable to that of producing biomass from higher plants. For example, potato can yield approximately 20000 kg of starch per hectare, with the potato tuber accumulating starch up to 80% of its dry weight (Martin, J. H., Leonard, W. H. and

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Stamp, D. L. (eds), Chapter 36, In: Principles of Field Crop Production, 898-932, Macmillan, New York, 1976). Starch is one of the lowest priced (approximately \$0.2/kg) and most abundant worldwide commodities. Similarly, oil producing crops, such as rapeseed, produce 1000 kg of oil per hectare with seed oil content up to 44% dry weight (Downey, R. K. and Röbbelen, G., In: Oil crops of the world, Röbbelen, G., Downey, R. K. and Ashri, A. (eds), Chpt. 16, McGraw-Hill, New York, 1989). In addition to be highly productive, plants have been shown to be very effective in producing a number of biologically active foreign proteins, such as antibodies (Hiatt, A., Cafferkey, R. and Bowdish, K., Nature 342: 76-78, 1989). There is growing interest in making use of the high productivity and flexibility of plants to produce a variety of organic materials, including proteins and various other polymers (Moffat, A. S., Science 256: 770-771, 1992).

Production of poly D-(-)-3-hydroxybutyrate, one member in the family of PHAs, has previously been demonstrated in the higher plant *Arabidopsis thaliana* (Poirier, Y., Dennis, E., Klomparens, K. and Somerville, C., Science 256: 520-523, 1992 and patent application Serial No. 07/732,243). Of the three enzymes required to make PHB from acetyl-CoA, the 3-ketothiolase is endogenously present in plants. In the initial experiments, the genes from the bacterium *Alcaligenes eutrophus* encoding 3-ketothiolase (*phbA*), the acetoacetyl-CoA reductase (*phbB*) and the PHB synthase (*phbC*) were transferred and expressed in *Arabidopsis* under the transcriptional control of the constitutive CaMV 35S promoter (Figure 1). In these experiments, the enzymes were targeted to the cytoplasm, because of the absence of organelle targeting signals on the gene products. Through appropriate genetic crosses, a hybrid plant was obtained which contained all of the enzymes required for PHB synthesis. Analysis of the chloroform-



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soluble compounds present in the hybrid plant by gas chromatography and mass spectrometry (GC-MS) revealed the presence of PHB. Between 20 to 100  $\mu$ g of PHB per gram fresh weight of plant material could be detected. Examination by electron microscopy of thin sections of plant tissues producing PHB revealed the presence of agglomerations of electron-lucent granules. These granules were very similar in size and appearance to the granules found in *A. eutrophus* and other bacteria accumulating PHB. Surprisingly, PHB granules were found in various compartments, namely the nucleus, vacuole and cytoplasm. No PHB granules could be detected in the mitochondria or chloroplast. The basis for this distribution of granules is unknown.

The demonstration of PHB production in genetically engineered *Arabidopsis* plants revealed several problems. One of the problems is the low yield of PHB. A second problem is the adverse effect of the expression of the *phb* genes on plant growth. Expression of high amounts of acetoacetyl-CoA reductase activity in transgenic plants caused a significant reduction in growth and seed production relative to wild type plants. For example, in a transgenic line expressing approximately 9 units of acetoacetyl-CoA reductase activity per mg of protein (one unit being defined as one  $\mu$ mole of acetoacetyl-CoA reduced per min), the fresh weight of 22 day-old shoots was reduced to 19% of wild type (Poirier, Y., Dennis, D.E., Klomparens, K., Nawrath, C. and Somerville C., FEMS Microbiol. Lett., 103: 237-246, 1992). Seed production was reduced in approximately the same proportion. This phenotype could be the result of the diversion of a significant amount of acetyl-CoA and/or acetoacetyl-CoA away from essential biochemical pathways leading to a decrease in the production of compounds such as phytohormones, carotenoids, sterols, quinones, flavonoids, and lipids (Figure 2). Alternatively, accumulation of  $\beta$ -

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hydroxybutyryl-CoA, or of a product derived from it, may be deleterious to plant cells. The fate of D- $\beta$ -hydroxybutyryl-CoA produced in transgenic plants is unknown. Expression of the PHB synthase, by itself, had no apparent effect on the growth or vigor of transgenic plants. However, hybrid plants containing both genes were more severely stunted in growth than plants containing only the acetoacetyl-CoA reductase activity. This could be due either to a more severe depletion of substrate from the mevalonate pathway or to a noxious effect of the PHB granules, particularly the granules being accumulated in the nucleus.

#### DESCRIPTION OF PREFERRED EMBODIMENTS

The present invention relates to a transgenic plant material having plastids, the plant material containing foreign DNA encoding a bacterial polypeptide which is selected from the group consisting of 3-ketothiolase, acetoacetyl-CoA reductase and polyhydroxyalkanoate (PHA) synthase and mixtures thereof leading to the production of a polyhydroxyalkanoate in the plastid in the plant.

The present invention also relates to a transgenic plant material having plastids, the plant material containing foreign DNA encoding a peptide which exhibits 3-ketothiolase activity in the plastid in the plant.

The present invention also relates to a transgenic plant material having plastids, the plant material containing foreign DNA encoding acetoacetyl-CoA reductase activity in the plastid of the plant.

The present invention also relates to a transgenic plant material having plastids, the plant material containing foreign DNA encoding a polypeptide which exhibits PHA synthase activity in the plastid of the plant.

The present invention also relates to a transgenic plant material having plastids, the plant

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material containing foreign DNA encoding one or more enzymes leading to the synthesis of polyhydroxyalkanoate (PHA) from hydroxyacyl-CoA in the plastid of the plant.

5 The present invention further relates to a transgenic plant material having plastids, the plant material containing foreign DNA encoding one or more enzymes which catalyze synthesis of hydroxyacyl-CoA in the plastid of the plant.

10 The present invention also relates to a transgenic plant having plastids, the plant material containing foreign DNA encoding one or more enzymes leading to production of acetoacetyl-CoA, from products encoded by the foreign DNA, in the plastid of the plant.

15 The present invention also relates to a transgenic plant material having plastids, the plant material containing foreign DNA encoding one or more enzymes leading to production of 3-hydroxybutyryl-CoA, from products encoded by the foreign DNA, in the plastid in the plant.

20 The present invention also relates to a method for introducing foreign DNA encoding polypeptides leading to the synthesis of a polyhydroxyalkanoate (PHA) in the plastid in a plant which comprises mating by sexual fertilization two plants which do not produce PHA, each containing foreign DNA from a bacterium  
25 encoding one or more different enzymes in a pathway leading to polymerization of hydroxyacyl-CoA by PHA synthase to produce the plant which synthesizes the PHA in a plastid of the plant.

30 OBJECTS

It is therefore an object of the present invention to provide one or more of the enzymes which lead to the accumulation of PHA, particularly PHB, in the plastid. It is further an object of the present  
35 invention to provide plants which exhibit good growth and seed formation. These and other objects will become increasingly apparent by reference to the following

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description and the drawings.

#### BRIEF DESCRIPTION OF DRAWINGS

Figure 1 is a flow diagram showing the pathway of PHB synthesis in *A. eutrophus*. The genes encoding the three enzymes are shown in parenthesis.

Figure 2 is a flow diagram showing metabolic pathways utilizing acetyl-CoA and acetoacetyl-CoA in transgenic plants producing PHB. The major end-products of endogenous plant metabolic pathways utilizing acetyl-CoA and acetoacetyl-CoA as precursors are shown in the upper part of the diagram. The additional pathway created in transgenic plants by the expression of the *phbB* and *phbC* genes from *A. eutrophus* is indicated in the box.

Figure 3 is a schematic diagram of the TPSS-*phb* gene fusions. a) TPSS-3-ketothiolase gene fusion, b) TPSS-acetoacetyl-CoA reductase gene fusion and c) TPSS-PHB synthase gene fusion.

All of these constructs are composed of four distinct regions indicated in boxes, namely the 55 amino acid transit peptide and the first 23 amino acids of the mature protein encoded by the gene 3.6 of the small subunit of Rubisco of pea, a short linker sequence and the full coding region of the *phbA* (A), *phbB* (B) and *phbC* (C) genes of *A. eutrophus* with exception of the initial methionines. The amino acid sequences (single letter code) in bold and DNA sequences present at the junctions of each region are indicated. Stretches of amino acids between the junctions, indicated by hyphens, have previously been published (Cashmore, A. R. In: Genetic engineering of plants (ed. Kosuge, T., Meredith, C.P. and Hollaender, A.) 29-38, Plenum Press NY, 1983; Janes, B., Hollar, J and Dennis, D., E. A. Dawes (ed.), Novel Biodegradable Microbial Polymers 175-190 (1990)). The stars indicate termination codons. Endonuclease restriction sites which were introduced by PCR during subcloning procedures are indicated.

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Figure 4 is a schematic diagram of the Ti-plasmids harboring the CaMV 35S promoter and TPSS-*phb* gene fusion. Maps of pBI-TPSS-Thio (A), pBI-TPSS-Red (B) and pBI-TPSS-Syn (C) are shown. The physical components of each constructs are, from left to right: LB, left border sequence; Kan, neomycin phosphotransferase II gene; CaMV-35S, cauliflower mosaic virus 35S promoter; TPSS, transit peptide of the small subunit (3.6 gene) of Rubisco of pea; hatch box, synthetic linker; 3-ketothiolase gene (A), acetoacetyl-CoA reductase gene (B), or PHB synthase gene (C); poly A, polyadenylation site; RB, right border sequence. The locations of important endonuclease restriction sites are indicated.

Figure 5 is a schematic diagram of the Ti plasmids harboring the seed specific promoter and TPSS-*phb* gene fusion. Maps of pBIB-CCN-Thio (A), pBIB-KCN-Red (B), and pBIB-HCN-Syn (C) are shown. For all the constructs, the seed specific promoter of the CRB gene of the 12S seed storage protein of *A. thaliana* was placed upstream of the TPSS-*phb* gene fusion. The following selectable marker were used: ALS encoding for acetolactate synthase (A), Kan, encoding for Neomycin phosphotransferase II; Hyg, Hygromycin phosphotransferase. Figure 4 shows a more detailed description.

Figure 6 is an autoradiograph of a Western blot analysis of transgenic *A. thaliana* plants expressing the plasmid pBI-TPSS-Thio and control plants. Aliquots of crude leaf protein extracts containing 1.2  $\mu$ g protein were separated on a 10% SDS-PAGE. Proteins electroblotted on nitrocellulose were incubated with anti-3-ketothiolase antibody. Protein extracts analyzed were T4-3A (lane C; Somerville, C. R., Poirier, Y., and Dennis, D. E., patent application Serial No. 07/732,243), TPSS-Thio GHI 1 (lane 1), TPSS-Thio L (lane 2), TPSS-Thio STU4 (lane 3), and TPSS-Red STU (lane U).

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Figure 7 is an autoradiograph of a Western blot analysis of transgenic *A. thaliana* plants expressing the plasmid pBI-TPSS-Red and control plants. Aliquots of crude leaf protein extracts containing 1.2  $\mu$ g protein were separated on a 12% SDS-PAGE. Proteins electroblotted on nitrocellulose were incubated with anti-acetoacetyl-CoA reductase antibody. Protein extracts analyzed were RedB-2B (lane C; Somerville, C. R., Poirier, Y., and Dennis, D. E., patent application Serial No. 07/732,243), TPSS-Red DEF (lane 1), TPSS-Red GHI1 (lane 2), TPSS-Red GHI2 (lane 3), TPSS-Red MNO1 (lane 4), TPSS-Red MNO2 (lane 5), TPSS-Red STU (lane 6), TPSS-Red VXY (lane 7), and TPSS-Syn VXY (lane U).

Figure 8 is an autoradiograph of a Western blot analysis of transgenic *A. thaliana* plants expressing the plasmid pBI-TPSS-Syn and control plants. Aliquots of crude leaf protein extracts containing 50  $\mu$ g protein were separated on a 8% SDS-PAGE. Proteins electroblotted on nitrocellulose were incubated with anti-PHB synthase antibody. Protein extracts analyzed were S8-1-2C (lane C, Somerville, C. R., Poirier, Y., and Dennis, D. E., patent application Serial No. 07/732,243), TPSS-Red STU (lane U), TPSS-Syn GHI1 (lane 1), TPSS-Syn GHI2 (lane 2), TPSS-Syn JKL (lane 3), and TPSS-Syn VXY (lane 4).

Figure 9 is an autoradiograph of a Western blot analysis of transgenic *A. thaliana* plants expressing the plasmid pBIB-CCN-Thio and control plants. Aliquots of crude seed protein extracts containing 50  $\mu$ g protein were separated on a 12% SDS-PAGE. Proteins electroblotted on nitrocellulose were incubated with anti-3-ketothiolase antibody. Protein extracts analyzed were CN-Red 17-1 (lane C), CN-Thio 13-3 (lane 1) and CN-Thio 14-1 (lane 2).

Figure 10 is an autoradiograph of a Western blot analysis of transgenic *A. thaliana* plants expressing the pBIB-KCN-Red and control plants. Aliquots

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of crude protein extracts containing 50  $\mu$ g protein were separated on a 12% SDS-PAGE. Proteins electroblotted on nitrocellulose were incubated with anti-acetoacetyl-CoA reductase antibody. Protein extracts analyzed were RedB-2B (lane LR; Somerville, C. R., Poirier, Y., and Dennis, D. E., patent application Serial No. 07/732,243), seed protein extracts were CN-Syn 34-1H1 (lane U), CN-Red 17-3K (lane 1) and CN-Red 17-1 (lane 2).

Figure 11 is an autoradiograph of a Western blot analysis of transgenic *A. thaliana* plants expressing the plasmid pBIB-HCN-Syn and control plants. Aliquots of crude protein extracts containing 50  $\mu$ g protein were separated on a 12% SDS-PAGE. Proteins electroblotted on nitrocellulose were incubated with anti-PHB synthase antibody. Protein extracts analyzed were S8-1-2C (lane LS; Somerville, C. R., Poirier, Y., and Dennis, D. E., patent application Serial No. 07/732,243), RedB-2B (lane LR; Somerville, C. R., Poirier, Y., and Dennis, D. E., patent application Serial No. 07/732,243), CN-Red 17-1 (lane C), CN-Syn 35-1 (lane 1), CN-Syn 35-1aA (lane 2), CN-Syn 35-G1 (lane 3), CN-Syn 34-1 Hb (lane 4), CN-Syn 34-1 Hc (lane 5), CN-Syn 34-1bA (lane 6), CN-Syn 34-1bA2 (lane 7), CN-Syn 34-1bB (lane 8), CN-Syn 34-1B (lane 9), and CN-Syn 34-1G (lane 10).

Figure 12 is an autoradiograph of a Southern blot analysis of untransformed control and transgenic *A. thaliana* plants transformed with the plasmid pBI-TPSS-*phb* constructs. One  $\mu$ g of genomic DNA from untransformed *A. thaliana* race Rschew and from transgenic plants were digested with the restriction enzyme HindIII, the fragments were separated by agarose gel electrophoresis and transferred to nylon membranes. Filters were hybridized to  $^{32}$ P-labeled DNA fragments from genes (A) *phbA*, (B) *phbB* and (C) *phbC*. The genomic DNAs analyzed were TPSS-Thio GHI1 (lane Thio 1), TPSS-Thio L

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(lane Thio 2), TPSS-Thio STU4 (lane Thio 3), TPSS-Red DEF (lane Red 1), TPSS-Red GHI1 (lane Red 2), TPSS-Red GHI2 (lane Red 3), TPSS-Red MNO1 (lane Red 4), TPSS-Red MNO2 (lane Red 5), TPSS-Red STU (lane Red 6), TPSS-Red VWX (lane Red 7), TPSS-Syn GHI1 (lane Syn 1), TPSS-Syn GHI2 (lane Syn 2), TPSS-Syn JKL (lane Syn 3), TPSS-Syn VWX (lane Syn 4) and untransformed wild type (lane C).

Figure 13 is an autoradiography of a Southern blot analysis of untransformed control and transgenic *A. thaliana* plants transformed with the plasmid pBIB-CN-*phb* constructs. The genomic DNAs analyzed were CN-Thio 13-3 (lane Thio 1), CN-Thio 14-1 (lane Thio 2), CN-Red 17-2 (lane Red 1), CN-Red 17-3 (lane Red 2), CN-Red 17-1dA (lane Red 3), CN-Red 17-1dB (lane Red 4), CN-Red 17-3K (lane Red 5), CN-Red 17-2K (lane Red 6), CN-Syn 34-1bA (lane Syn 1), CN-Syn 34-1bB (lane Syn 2), CN-Syn 34-1Hb (lane Syn 3), CN-Syn 34-1G1 (lane Syn 4), CN-Syn 35-1 (lane Syn 5), CN-Syn 35-1A (lane Syn 6), and untransformed wild type (lane C). Refer to figure legend 12 for a more detailed description.

Figure 14 shows gas chromatography (GC) analysis of purified PHB and plant extracts. (A) Gas chromatogram of transesterified PHB purchased from Sigma Chemical Company; (B) Gas chromatogram of chloroform extracts of leaves from untransformed wild type *A. thaliana* race Rschew. The arrow shows the position where ethyl-hydroxybutyrate would elute from the chromatogram; (C) Gas chromatogram of chloroform extracts of leaves from hybrid TPSS-Thio L/TPSS-Red DEF/TPSS-Syn GHI1. The arrow indicates the location of the ethyl-hydroxybutyrate peak.

Figure 15 shows gas chromatography-mass spectrometry analysis of ethyl-hydroxybutyrate prepared from a PHB standard and PHB from plant extracts. (A) Mass spectrum of transesterified commercial PHB; (B) mass spectrum of the GC peak from leaf chloroform extract of a TPSS-Thio L/TPSS-Red DEF/TPSS-Syn GHI1



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hybrid having a retention time identical to ethyl-hydroxybutyrate (as shown in Figure 14 C).

5 Figure 16 shows bar graphs illustrating the PHB accumulation in leaves of different hybrid TPSS-Thio/TPSS-Red/TPSS-Syn plants. (A) measurements made on expanding leaves (20-30 day-old); (B) measurements made on mature leaves (50-60 day-old).

10 Figure 17 shows pictures of fully developed rosettes of wild type (WT) and transgenic *Arabidopsis* plants expressing the PHB biosynthetic enzymes in the plastid (A) and in the cytoplasm (B). The leaves of the hybrid TPSS-Thio L/TPSS-Red DEF/TPSS-Syn-GHI1 producing PHB in the plastid contained approximately 1.2 mg PHB/g fresh weight (A, PHB+). The Red/Syn hybrid expressing  
15 the PHB enzymes in the cytoplasm contained approx. 100  $\mu$ g PHB/g fresh weight (B/PHB+). Wild type and transgenic plants were grown under identical conditions.

20 Figure 18 shows a picture illustrating the effect of high level accumulation of PHB in the plastid on leaf pigmentation. (A) Leaf of a 50 day old wild type plant; (B) Leaf of a 50 day old transgenic *Arabidopsis* hybrid producing 700  $\mu$ g PHB/g fresh weight in the plastid of expanding leaves.

25 Figure 19 shows transmission electron micrographs (TEM) of thin sections from a PHB-producing tri-hybrid expressing the PHB enzymes in the plastid (TPSS-Thio L/TPSS-Red DEF/TPSS-Syn GHI1). (A) Agglomeration of electron-translucent granules in the chloroplast of a mesophyll cell is indicated by the  
30 arrows. The plant was put in the dark for 48 h before sampling for EM analysis in order to remove the starch. Bar represent 1  $\mu$ m. (B) Transmission electron micrographs of thin sections of wild type leaves collected after 4 hours of illumination in a 12 h  
35 photoperiod. Starch accumulation in the plastids in form of oval singular granules are indicated by large arrows in wild type; (C) Transmission electron

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micrographs of thin sections of PHB-positive TPSS-Thio L/TPSS-Red DEF/TPSS-Syn GHI1 hybrid leaves collected after 4 hours of illumination in a 12 h photoperiod. Starch accumulation in the plastids in form of ovular singular granules are indicated by large arrows. Agglomerations of electron-lucent PHB granules in the plastid of the tri-hybrid are indicated by small arrows. Bars represent 1  $\mu$ m.

Figure 20 shows a Western blot analysis of protein extracts of transgenic TPSS-Thio L/TPSS-Red DEF/TPSS-Syn GHI1 plants incubated with the anti-PHB synthase antibody. Extracts of soluble proteins (Lanes 1, 2) and of solubilized proteins of the membrane and particulate fraction (Lanes 3, 4) of two different TPSS-Thio L/TPSS-Red DEF/TPSS-Syn GHI1 plants. Lane-C shows extract of soluble proteins of a TPSS-Syn GHI1 plant.

It is helpful to set forth definitions of certain terms to be used hereinafter.

Transformation means the process for changing the genotype of a recipient organism by the stable introduction of DNA by whatever means.

A transgenic plant is a plant which contains DNA sequences which are not normally present in the species, but were introduced by transformation.

Transcription means the formation of an RNA chain in accordance with the genetic information contained in the DNA.

Translation means the process whereby the genetic information in an mRNA molecule directs the order of specific amino acids during protein synthesis.

A promoter is a DNA fragment which causes transcription of genetic material. For the purposes described herein, promoter is used to denote DNA fragments that permit transcription in plant cells.

A poly-A addition site is a nucleotide sequence which causes certain enzymes to cleave mRNA at a specific site and to add a sequence of adenylic acid

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residues to the 3'-end of the mRNA.

5        *phbC*, *phbA*, *phbB* are the gene symbols given to  
the *A. eutrophus* genes for PHB polymerase, 3-  
ketothiolase and acetoacetyl-CoA reductase, respectively  
(Peoples, O. P. and Sinskey, A. J., J. Biol. Chem 264:  
15298-15303, 1989).

10        A plastid is a self-replicating organelle  
which is located in multiple copies in the cytoplasm of  
different kinds of plant cells. This organelle is  
surrounded by a double layered membrane and contains its  
own DNA. Proteins located in the plastid are either  
15        encoded by its own DNA and synthesized in the plastid or  
are encoded by the nucleus of the plant cell,  
synthesized in the cytoplasm and transported into the  
plastid.

20        In describing the progeny of transgenic  
plants, it is useful to adopt a convention which  
designates how many generations of self-pollination have  
elapsed since the introduction of DNA. Herein, we  
designate the original transformant the T0 generation.  
The progeny resulting from self-pollination of this  
generation is designated the T1 generation and so on.

25        In the case of cross-pollination between two  
distinct parental plants, the resulting progeny from the  
initial cross-pollination event is designated the F1  
generation.

30        The invention described in this disclosure  
concerns the alleviation of the growth disruption and  
low PHB production associated with the first generation  
of PHB producing plants by changing the cellular  
localization of the PHB biosynthetic enzymes and by  
regulating the tissue specificity and the timing of  
expression.

35        In order to both increase PHB production and  
avoid the potential depletion of essential products  
derived from acetyl-CoA and/or acetoacetyl-CoA, the  
bacterial PHB biosynthetic enzymes were targeted to a

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subcellular compartment having a high metabolic flux through acetyl-CoA and/or acetoacetyl-CoA, namely the plastid. Being the site of fatty acid synthesis in plants, the plastid has a high level of acetyl-CoA production (Harwood, J. L., Ann. Rev. Plant Physiol. Plant Mol. Biol. 39: 101-138, 1988). In storage tissues, diversion of some of this plastid acetyl-CoA away from fatty acid biosynthesis toward PHB production should not be deleterious to the growth of the plant. Starch, a high molecular weight biopolymer naturally synthesized in plants, accumulates to a high amount in the plastids of many storage tissues (amyloplasts) (Preiss, J., Ann. Rev. Plant Physiol. 33: 431-454, 1982). In photosynthetic chloroplasts, starch also accumulated transiently during the daily period of CO<sub>2</sub>-fixation. The plastid is therefore a compartment which can vary its dimensions and has a large storage capacity. Thus, the accumulation of PHB in the plastid is not expected to interfere with the plastid function or cause some mechanical disruption. Furthermore, expression of the PHB biosynthetic pathway in the cytoplasm resulted in PHB granule accumulation in the cytoplasm, nucleus and vacuole, but not in the plastid (Poirier, Y., Dennis, E., Klomparens, K. and Somerville, C. Science 256: 520-523, 1992). This raises the possibility that the plastid envelope is impervious to penetration by PHB granules. Therefore, an added advantage of plastid PHB production is that PHB granules may accumulate and remain exclusively in the plastid, avoiding potential mechanical disruption of other organelles by the granules.

In the invention described here, the genes *phbA*, *phbB* and *phbC* from *Alcaligenes eutrophus* modified for plastid targeting of the encoded enzymes were introduced into plant cells. They were expressed under the transcriptional control of the CaMV 35S promoter, the same promoter which had been used previously to

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construct PHB producing plants. This approach allows a direct comparison of the plastid and cytoplasmic expression of the enzymes and of the PHB production levels.

5 In a second part of the invention described here, PHB production was restricted to a specific tissue and a specific stage of the plant life cycle to reduce the possibility of deleterious effects on the overall growth of the plants. Since the flux of acetyl-CoA in  
10 the plastids is particularly high in tissues which normally accumulate a large amount of oil, such as the seeds of an oil plant, the developing seed is a suitable tissue for the PHB production. The diversion of some of this acetyl-CoA away from fatty acid synthesis used for  
15 storage lipids towards PHB synthesis should not be deleterious for the growth of the plant. Therefore, the plastid targeted *phb* enzymes were expressed specifically in the developing seeds using the promoter of a seed storage protein gene of *Arabidopsis thaliana*.

20 PHA production on an agricultural scale requires that the PHA producing plants have normal vigor and that the level of PHA produced be above a certain minimum level which has not yet been reached in previous generations of transgenic plants. This invention is  
25 therefore of high importance for the successful development of PHA producing plants. Because of the close relationship of *Arabidopsis* and *Brassica napus*, the constructs described in the following sections could be directly used for PHB production in *Brassica*. In  
30 addition, because of the similarity in mechanisms of gene expression and primary carbon metabolism in different species of higher plants, it is also apparent that the essence of this invention, the production of PHA in plastids, is applicable to other plant species.  
35 The production of PHB in other oil-producing plants, such as the seeds of rape and sunflower or in the mesocarp of avocado or oilpalm, are particularly

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attractive since these plant organs are specialized on providing the precursor acetyl-CoA for fatty acid biosynthesis.

Although the experiments discussed hereinafter concern the plant species *Arabidopsis thaliana* (L.) Heynhold, the process described is generally applicable to any higher plant for which a method of transformation is available. Similarly, although the process described herein concerns the use of genes from *A. eutrophus*, the process described is generally applicable to the use of genes from any organism which is capable of synthesis of PHB. It is also clear that, although the process described concerns the production of PHB, the procedure is generally applicable to the production of any polyhydroxyalkanoate which is normally produced in microorganisms by the activity of PHA synthase (which includes PHB synthase), and for which the appropriate hydroxyacyl-CoA substrate is produced in the particular plant.

The production of PHB in the plastids in transgenic plants requires the completion of a sequence of steps as follows:

- 1.) the construction of one or more plasmids containing fusions of the bacterial genes for PHB synthesis to plastid targeting sequences expressed under the control of a plant promoter in *E. coli*,
- 2.) the introduction of these plasmids into *Agrobacterium tumefaciens*
- 3.) the infection of plants with the transformed *Agrobacterium tumefaciens* in order to transform plant cells with the modified genes (i.e., *A. thaliana* in this example)
- 4.) the selection of plants transformed with the modified genes,
- 5.) the selection of plants which are homozygous for the ectopic genes,
- 6.) analysis of the transformed plants concerning integration of the plasmid and the expression of the ectopic genes to ensure that they are active and that the gene products are targeted to the plastid, processed and functional,
- 7.) the production of

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hybrid plants containing two or more different ectopic genes by sexual crosses, 8.) the analysis of the hybrid material for the presence of PHB.

5           1. Construction of the plasmids containing the plastid targeting sequence - *phb* gene fusions under the control of a plant promoter in *E. coli*.

1. 1. Fusion of a signal sequence to the coding regions of the *phb* genes.

10           In order to target a protein to the stroma of the plastid in plant cells, the protein must contain a transit peptide at its N-terminal end (Keegstra, K. and Olsen, L. J., Annu. Rev. Plant Physiol. Plant Mol. Biol, 40: 471-501, 1989; Archer, E. K. and Keegstra, K., J. Bioenerg. Biomem., 22: 789-810, 1990). Therefore, a  
15           signal sequence encoding the transit peptide has to be fused in the correct reading frame to the 5' end of the coding sequence of the protein. The transit peptide of the small subunit of the ribulose 1-5 biphosphate  
20           carboxylase (rubisco) (TPSS) has been well characterized (Robinson, C. and Ellis, R. J., Eur. J. Biochem, 142: 343-346, 1984, Wasmann, C. C., Reiss, B., Barlett, S. G., and Bohnert, H. J., Mol. Gen. Genet. 205: 446-453, 1986; Friedmann, A. L. and Keegstra, K., Plant Physiol.  
25           89: 993-999, 1988; Lubben, T. H., Gatenby, A. A., Ahlquist, P., and Keegstra, K., Plant Mol. Biol. 12: 13-18, 1989; Schnell, D. J., Blobel, G., and Pain, D., J. Biol. Chem. 266: 3335-3342, 1991) and has been  
30           previously used successfully in a number of targeting experiments (van de Broeck, G., Timko, M. P., Kausch, A. P., Cashmore, A. R., Van Montagu, M. and Herrera-Estrella, L., Nature 313: 358-363, 1985; Schreier, P. H., Seftor, E. A., Schell, J., and Bohnert, H. J., EMBO J. 4: 25-32, 1985; Boutry, M., Nagy, F., Poulsen, C.,  
35           Aoyagi, K., and Chua N.-H., Nature 328: 340-342, 1987; Lubben, T. H., and Keegstra, K., Proc. Natl. Acad. Sci 83: 5502-5506, 1986; Lamppa, G. K., J. Biol. Chem, 263:

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14996-14999, 1988; Gatenby, A. A., Lubben, T. H., Ahlquist, P., and Keegstra, K., EMBO J. 7: 1307-1314, 1988; Cheung, A. Y., Bogorad, L., Van Montagu, M., and Schell, J., Proc. Natl. Acad. Sci. 85: 391-395, 1988; 5 Lubben, T. H., Theg, S. M. and Keegstra, K., Photosyn. Res. 17: 173-194, 1988). The TPSS of pea was therefore used in the following experiments. However, a number of different transit peptides involved in plastid targeting could also be used in an analogous way.

10           Since the transit peptide is normally cleaved off during the import into the plastid, the 3-dimensional structure at the junction between the transit peptide and the protein may be important for the efficiency of the transport (Wasmann, C. C., Reiss, B., 15 Barlett, S. G., and Bohnert, H. J., Mol. Gen. Genet. 205: 446-453, 1986; Lubben, T. H., Gatenby, A. A., Ahlquist, P., and Keegstra, K., Plant Mol. Biol. 12: 13-18, 1989). Therefore, the sequence of the gene encoding the first 23 amino acids of the mature small subunit of 20 rubisco was included in the transit peptide, which was fused to the bacterial genes of *A. eutrophus* involved in PHB production, namely the *phbA*, *phbB* and *phbC* genes.

          To obtain the exact fusion between the signal sequences and the bacterial genes, the sequences coding 25 for the TPSS as well as *phb* genes were amplified by polymerase chain reaction (PCR) using oligonucleotide primers which created new synthetic restriction sites at either end of the sequence. The primers designed for amplification are presented in Table 1.



Table 1. PCR-amplifications

	Oligonucleotide	introduced site a	DNA source	fragment size b
<i>phbA</i> gene				
5' side	5' CATCCCGGGTGATGACGTTGTCATC 3'	SmaI SacI	pUC-Thio c	1.3 kb
3' side	5' GAATTCGAGCTCGGTACCCCTGAGTC 3'			
<i>phbB</i> gene				
5' side	5' AATCCCGGGTGACTCAGCGCATTGCG 3'	SmaI SacI	pUC-Red c	0.8 kb
3' side	5' GAATTCGAGCTCGGTACCGCGGCTGC 3'			
<i>phbC</i> gene				
5' side	5' AATCCCGGGTGGGGAACCGGCAAAGGC 3'	SmaI SmaI	pUC-Syn c	1.9 kb
3' side	5' CTACCCGGGAAGCGTCATGCCTTGGC 3'			
TPSS cod. region				
5' side	5' CCGTCTAGAATGGCTTCTATGATATCCT 3'	XbaI SmaI	TPSSNPTII d	0.27 kb
3' side	3' GCAACCCGGGAATCTCTGGTCAATGGTGG 5'			
CRB promoter				
5' side	5' CTCTCTAGAAGTGGGAAGCACTCGAG 3'	XbaI XbaI	nA14011 e	1.1 kb
3' side	5' CGGTCTAGATCCTCTTTATTGATTACT 3'			

a) Restriction site introduced using the oligonucleotide for PCR reaction.

b) Size of the amplified DNA fragment using the oligonucleotides and DNA source.

c) Somerville, C. R., Poirier, Y. and Dennis, D. E., patent application serial no. 07/732,243.

d) Wasmann, C. C., Reiss, B., Barlett, S. G., and Bohnert, H. J., Mol. Gen. Genet. 205: 446-453, 1986.

e) Pang, P. P., Pruitt, R. E. and Meyerowitz, E. M., Plant Mol. Biol. 11: 805-820, 1988.

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Table 1 also includes the source of the DNA from which the fragments were amplified and the size of the amplified fragment. The PCR fragments were purified, cleaved with enzymes recognizing the introduced restriction sites and separated by agarose gel electrophoresis.

The purified 0.27 kbp *XbaI*-*SmaI* fragment containing the DNA fragment of the signal sequence was ligated to the vector pUC18 cleaved with the same restriction enzymes to produce the plasmid pUC-TPSS.

The purified 1.3 kbp *SmaI*-*SacI* fragment of the *phbA* gene and the 0.8 kbp fragment of the *phbB* genes were ligated into the *SmaI* and *SacI* cut pUC-TPSS plasmid to create the plasmids pUC-TPSS-Thio and pUC-TPSS-Red. The 1.9 kbp *SmaI* fragment of the *phbC* gene was ligated to pUC-TPSS cut with *SmaI*. A clone in which the synthase was cloned in the correct orientation behind the signal sequence was selected and designated pUC-TPSS-Syn.

In summary, each of the created plasmids, namely pUC-TPSS-Thio, pUC-TPSS-Red and pUC-TPSS-Syn, contains a part of a coding region of a plant gene and of a bacterial gene fused together in a way that they code for one synthetic polypeptide. At the junction between the plant and the bacterial sequence a synthetic sequence was formed coding for the three amino acids serine-arginine-valine (S-R-V). The amino acid and DNA sequences present at the junctions between the signal sequences and the bacterial genes are shown in Figure 3. When expressed in a plant cell, these polypeptides are expected to be recognized by the protein import machinery of the plastids and transported to the stroma of the plastids.

1. 2. Addition of a plant promoter upstream of the modified *phb* genes.

In order to obtain transcription of synthetic

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coding regions in higher plants, coding regions have to be under the control of a plant promoter located near the 5' end of the coding region. In addition, it is common practice to add a polyadenylation site to the 3' end of the coding region in order to ensure proper expression of the gene in higher plants. Furthermore, for the selection of transformed plants, a gene has to be present which enables only transformed plants to survive under selecting conditions. Such a gene is called a selectable marker. Two different promoters were used to express the modified *phb* genes: the CaMV 35S promoter and the CRB promoter.

The CaMV 35S promoter (from cauliflower mosaic virus) is regarded as a constitutive promoter which results in relatively high levels of transcription in a wide variety tissues in many species of higher plants (Benfey, P. N. and Chua, N.-H., Science 250: 959-966, 1990). In contrast, the CRB promoter isolated from the CRB gene of the 12S seed storage protein of *Arabidopsis thaliana* promotes high levels of transcription almost exclusively in the embryo of developing seeds (Pang, P. P., Pruitt, R. E., and Meyerowitz, E. M., Plant Mol. Biol. 11: 805-820, 1988).

1.2.1. Addition of the CaMV 35S promoter upstream of the modified *phb* genes.

In order to place the CaMV 35S promoter upstream of the modified *phbA*, *phbB* and *phbC* genes and to fulfill the other requirements for the expression of a coding region in higher plants, the plasmid vector pBI121 (Clontech, CA) was used. This vector contains the neomycin II phosphotransferase gene as a selectable marker.

To construct the CaMV 35S-TPSS-*phbA* and the CaMV 35S-TPSS-*phbB* gene fusions, the plasmids pUC-TPSS-Thio and pUC-TPSS-Red were digested with the restriction enzymes XbaI and SacI. The 1.6 kbp

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restriction fragment from pUC-TPSS-Thio and the 1.1 kbp fragment from pUC-TPSS-Red were separated from the other fragments by agarose gel electrophoresis. The purified DNA fragments were ligated to pBI121 cleaved with the same enzymes and cloned into *E. coli*. The newly created plasmids pBI-TPSS-Thio and pBI-TPSS-Red contain the *phbA* gene and the *phbB* gene, respectively, modified for plastid targeting and located downstream of a plant promoter (Figure 4).

To construct the CaMV 35S-TPSS-*phbC* gene fusion, the plasmid pUC-TPSS-Syn was digested with EcoRI and the staggered ends were filled by T4 DNA polymerase. The plasmid was subsequently digested with XbaI. A 2.2 kbp DNA fragment was separated from other fragments by agarose gel electrophoresis. The purified DNA fragment was cloned into pBI121 cleaved by the restriction enzyme SmaI/XbaI. The resulting plasmid, designated pBI-TPSS-Syn (Figure 4), has the *phbC* gene from *A. eutrophus* modified for plastid targeting cloned in the right orientation, relative to the CaMV promoter and the polyadenylation site of pBI121, so that it is expected to be expressed in higher plants.

These constructs are expected to satisfy all requirements for high expression of the genes and targeting of the corresponding proteins, namely the modified 3-ketothiolase, the modified acetoacetyl-CoA reductase and the modified *phb* synthase, to the stroma of the plastid.

1.2.2. Addition of the seed specific promoter upstream of the modified *phb* genes.

For cloning of the modified *phb* coding regions downstream of the CRB promoter, the pBIB vectors (Becker, D., Nucleic Acids Res. 18: 203, 1990) were used. These vectors contain all functions that are needed for plant transformation. There are two versions of the vector: pBIB-Kan carries the neomycin II

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phosphotransferase gene as selectable marker, pBIB-Hyg the hygromycin phosphotransferase gene.

In order to simplify the subsequent cloning procedure, the CRB promoter had to be slightly modified by the removal of the XbaI restriction site at position -993. Therefore the plasmid nAt4011 (Pang P. P., Pruitt, R. E. and Meyerowitz, E. M., Plant Mol. Biol. 11: 805-820, 1988) was digested with BamHI and EcoRI and after purification the 3.5 kbp fragment was cloned into pBR322 (Bolivar, F., Rodriguez, R. L., Greene, P. J., Betlach, M. C., Heyneker, H. L. and Boyer, H. W., Gene 2: 95-113, 1977) to produce pBR322-CRB. After cutting the single XbaI site of pBR322-CRB, the staggered ends were filled in with deoxyribonucleotides by incubation with T4 DNA polymerase, and the plasmid was religated. The resulting plasmid contained no XbaI site in the CRB promoter region.

In order to obtain the CRB promoter with suitable restriction sites at either end of the sequence, a polymerase chain reaction was performed by using oligonucleotide primers indicated in Table 1. The 1.1 kbp XbaI fragment was cloned into pK19 (Pridmore, R. D., Gene 56: 309-312, 1987) to create pK-CRB.

In order to clone the TPSS-*phbA* coding region behind the CRB promoter, the plasmid pUC-TPSS-Thio was digested with the restriction enzymes XbaI and SacI and the 1.6 kbp DNA fragment was purified by agarose gel electrophoresis. This fragment was ligated to the vector pBIB-Hyg cleaved by XbaI and SacI. Since it would be very useful to have a different selectable marker combined with each of the three *phb* genes, the hygromycin II phosphotransferase gene of the pBIB-Hyg vector was subsequently replaced by the acetolactate synthase gene, which confers chlorsulfuron resistance to transformed plants (Haughn, G. W., Smith, J., Mazur, B. and Somerville C. R., Mol. Gen. Genet. 211: 266-271, 1988). To do this, the resulting plasmid was cleaved by

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HindIII and BamHI to remove the hygromycin II phosphotransferase gene. The staggered ends of the plasmid were filled with deoxyribonucleotides by T4 DNA polymerase. The purified 5.8 kbp XbaI fragment from the plasmid pGH1 (Haughn, G. W., Smith, J., Mazur, B. and Somerville C. R., Mol.Gen. Genet. 211: 266-271, 1988) was subsequently inserted in the prepared plasmid. The resulting construct was designated as pBIB-C-TPSS-Thio. The CRB promoter was then added to the construct by cloning the 1.1 kbp long XbaI fragment of pK-CRB into the unique XbaI site of pBIB-C-TPSS-Thio. A clone containing the promoter in the right orientation for proper expression of the modified *phbA* was designated as pBIB-CCN-Thio (Figure 5).

In order to clone the TPSS-*phbB* coding region behind the CRB promoter, the plasmid pUC-TPSS-Red was digested with XbaI and the 1.1 kbp XbaI fragment of the plasmid pK-CRB was inserted. A clone with the promoter in the right orientation was selected and designated as pK-CN-Red. The plasmid pK-CN-Red was digested with EcoRI and PstI to obtain the promoter/gene fragment and the ends were filled in with deoxyribonucleotides by T4 DNA polymerase. The 2.2 kbp fragment was purified by agarose gel electrophoresis and ligated in the vector pBIB-Kan digested with SmaI. A clone having the fragment in the right orientation for a proper gene expression in plants was named pBIB-KCN-Red (Figure 5).

In order to clone the TPSS-*phbC* coding region behind the CRB promoter in the pBIB-Hyg vector, the plasmid pUC-TPSS-Syn was digested with EcoRI, the staggered ends were filled by T4 DNA polymerase and the linearized plasmid was subsequently cut with XbaI. A 2.2 kbp DNA fragment was separated from other fragments by agarose gel electrophoresis. The purified DNA fragment was cloned into pBIB-Hyg digested with the restriction enzymes XbaI and SmaI. In this resulting plasmid digested with XbaI, the 1.1 kbp XbaI fragment containing

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the CRB promoter obtained by cleaving the plasmid pk-CRB was cloned. A clone which had the promoter in the right orientation for a proper expression of the modified *phbC* gene was designated as pBIB-HCN-Syn (Figure 5).

5 In summary, the plasmids pBIB-CCN-Thio, pBIB-KCN-Red, pBIB-HCN-Syn are constructed such that when transformed into plants, the modified genes will be specifically expressed in the developing seeds with the proteins being targeted to the stroma of a plastid in  
10 the seed.

## 2. Introduction of the constructs into *Agrobacterium tumefaciens*.

To enable the use of a plant transformation method which is mediated by *Agrobacterium tumefaciens*,  
15 the plasmids of both series of constructs were transferred into *Agrobacterium tumefaciens* strain pGV3101 by electroporation (Koncz, C. and Schell, J., Mol. Gen. Genet. 204: 383-396, 1986; Sambrook, J. Fritsch, E. F. and Maniatis, T. Molecular cloning, a  
20 laboratory manual, Cold Spring Harbor Laboratory Press, 1989). Bacterial colonies transformed with the various plasmids were recovered by selection for bacterial expression of the kanamycin resistance gene present on  
25 the plasmid pBI121 and pBIB.

## 3. Transformation of plant cells with *Agrobacterium tumefaciens*.

In the disclosed experiments, *Arabidopsis thaliana* was used as a model plant to show PHB  
30 production in the plastid. *A. thaliana* can be transformed by a *Agrobacterium tumefaciens* mediated meristem transformation method (Chang, S. S., Perk, S. K. and Nam, H.-G., Abstract in: Fourth International  
35 Conference on Arabidopsis Research, Vienna, 1990).

*Arabidopsis thaliana* race Rschew plants were grown under continuous light until the plants started

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bolting (approximately 3 weeks). The bolts (approx. 2 cm) were removed at their base together with the auxiliary buds. The wounded site was infected by *Agrobacterium* carrying the desired plasmid. Plants were grown until new bolts raised (approx. 1 week). Again the bolts were removed and the wounded site was infected with *Agrobacterium*. The plants were grown to full maturity and the seeds were harvested.

10

#### 4. Selection of transformed plants.

Transformed T0 plants were selected by distributing the seeds obtained from the plants infected with the various *Agrobacterium* strains on agar-solidified plant medium containing the appropriate selection compound. For the selection of transformed plants carrying the T-DNA of pBI-TPSS-Thio, -Red and -Syn and of pBIB-KCN-Red, 50µg/ml Kanamycin was added to the medium. For the selection of transformed plants carrying the T-DNA of pBIB-CCN-Thio, 30 ng/ml Chlorsulfuron was added to the medium and 30µg/ml Hygromycin for the selection of plants carrying pBIB-HCN-Syn. The above concentrations of the selection compounds prevent the growth of untransformed *A. thaliana* but permit normal growth of transformed plants. On average, from the seeds of approx. 40 plants infected with *Agrobacterium* one putative transformant could be isolated. Kanamycin resistant plants were designated with a letter/number combination.

A total of 14 kanamycin-resistant plants were recovered from seeds of plants which were infected with *A. tumefaciens* carrying the plasmid pBI-TPSS-Thio. These were designated TPSS-Thio GHI1, -GHI2, -GHI3, -GHI4, -L, -STU1, -STU2, -STU3, -STU4, -STU5, -STU6, -YZAA1, -YZAA2 and -YZAA3.

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A total of 10 kanamycin-resistant plant lines were recovered from seeds of plants which were infected with *A. tumefaciens* carrying pBI-TPSS-Red. These were



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designated TPSS-Red DEF, -GHI1, -GHI2, -MNO 1, -MNO 2, -P1, -P2, -QR, -STU, -VWX.

5 A total of 6 kanamycin-resistant plant lines were recovered from seeds of plants which were infected with *A. tumefaciens* carrying the plasmid pBI-TPSS-Syn. These were designated TPSS-Syn-ABC, -GHI1, -GHI2, -JKL, -PQR, -VWX.

10 A total of two chlorsulfuron resistant plants were recovered from seeds of plants which were infected with *A. tumefaciens* carrying the plasmid pBI-CCN-Thio. These were designated CN-Thio 13-3 and -14-1.

15 A total of 6 kanamycin-resistant plants were recovered from seeds of plants which were infected with *A. tumefaciens* carrying the plasmid pBI-KCN-Red. These were designated CN-Red 17-1, -17-3, -17-1dA, -17-1dB, -17-2K, -17-3K.

20 A total of 17 hygromycin-resistant plants were recovered from seeds of plants which were infected with *A. tumefaciens* carrying the plasmid pBI-HCN-Syn. These were designated CN-Syn 34-1bA, -34-1bB, -34-2 A, -34-2B, -34-1 Ha, -34-1 Hb, -34-1 Hc, -34-1G1, -34-1G2, -35-1, -35-1aA, -35-1aB, -35-2A, -35-2B, -35-2C, -35-3, -35-1G1.

5. Isolation of putative homozygous transgenic lines.

25 A minimum criterion used to produce homozygous transgenic lines was that all the progeny from an homozygous plant are expected to be resistant to the selection marker. Because the presence of multiple ectopic copies of the inserted T-DNA at different  
30 locations in the genome may cause a similar phenotype, this criterion is most useful when the primary transformation event involves insertion of T-DNA into only one chromosomal location.

35 In order to identify putative homozygous lines, the resistant T0 plants were grown to maturity in reproductive isolation. Subsequently several T1 plants shown to be resistant to the selection medium were again

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grown to maturity. The frequency of resistance to the selectable marker was then determined in samples of approximately 100 T2 seeds from each line. If all of the T2 seeds from a particular plant were resistant to the selectable marker, the line was provisionally considered to be homozygous.

6. Analysis of the transgenic plants obtained.

6.1. Analysis of the expression and the plastid targeting of the *phb* enzymes and their targeting to the plastid.

6.1.1. Analysis of putative transgenic plants obtained after transformation with pBI-TPSS-Thio, pBI-TPSS-Red and pBI-TPSS-Syn.

In order to determine whether the transgenic plants transformed with pBI-TPSS-Thio, pBI-TPSS-Red and pBI-TPSS-Syn produced functional enzymes located in the chloroplasts, proteins of the kanamycin resistant transgenic plants were analyzed by Western blot analysis. Western blots of proteins of transgenic plants transformed with pBI-TPSS-Thio were incubated with antibodies raised against the 3-ketothiolase of *A. eutrophus*. Western blots of proteins of transgenic plants transformed with pBI-TPSS-Red were incubated with antibodies raised against the acetoacetyl-CoA reductase and the proteins of transgenic plants transformed with pBI-TPSS-Syn were incubated with polyclonal antibodies from rabbits raised against the PHB synthase. As a negative control, an analysis of a protein extract of a transgenic plant not containing the putatively produced enzyme was included in the analysis. As a positive control, an extract of a transgenic plant producing the enzyme in the cytoplasm was included.

Of the 14 putative transgenic plants transformed with the pBI-TPSS-Thio, the protein extracts of the 3 plants, namely TPSS-Thio GHI1, -L and -STU4 showed a strong signal for the production of the

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3-ketothiolase (Figure 6). The enzyme appeared on the Western blot as a triplet of 45, 46.5 and 48 kDa bands. These bands represent the correctly processed protein and imprecisely processed products. The unmodified 3-ketothiolase located in the cytoplasm appears at 44 kDa. Therefore, the chloroplast targeted, correctly processed TPSS-3-ketothiolase is expected to have a molecular weight of ca. 47 kDa, because of the 23 amino acids added from the rubisco small subunit. The unprocessed protein, still harboring the entire transit peptide would have a molecular weight of ca. 53 kDa.

Of the 10 putative transgenic plants transformed with pBI-TPSS-Red, all plants except P1 and P2 showed a signal for the production of the acetoacetyl-CoA reductase. The intensity of these signals varied and was the strongest in TPSS-Red-DEF and -STU (Figure 7). The signal appeared always as a triplet of 28.5, 29.0 and 30.5 kDa bands representing the correctly processed and imprecisely processed forms of the protein. The unmodified protein migrates at 26.5 kDa. Therefore, an unprocessed TPSS-acetoacetyl-CoA reductase would be expected to have a molecular weight of 35 kDa and a correctly processed form of the protein would have a molecular weight of about 29 kDa.

All of the 6 putative transgenic plants transformed with pBI-TPSS-Syn except TPSS-Syn-ABC and -PQR showed a signal. The intensity of these signals varied and was the strongest in plant TPSS-Syn-VWX (Figure 8). The signal showed up as a triplet band at the size of the correctly processed TPSS-Syn protein (63 kDa), and a processed version slightly shorter than expected (60 and 61 kDa). The unmodified PHB Synthase migrates at 60 kDa.

In all Western blot analyses performed, proteins of untransformed plants showed no signal. Plants expressing the *phb* enzymes in the cytoplasm showed a strong signal at the expected size. The PHB

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enzymes modified with a transit peptide for targeting to the plastid were processed to the expected size and therefore mostly inserted into the plastid. In addition, bands at slightly higher or lower mobility also occurred. Proteins with a slightly higher mobility than expected might be generated by protease activity on the 23 amino acids of the mature protein of the small subunit of rubisco which were added to the bacterial enzymes. The artificially created extension might be especially susceptible to proteases.

These results indicate that for each construct containing the CaMV promoter, transformed plants could be obtained producing high levels of the expected enzymes. The appearance of each of these enzymes in the Western blot analyses as doublet or triplet of the expected sizes indicates that the enzymes are transported to the plastid and processed in the expected manner.

Transgenic plants obtained by transformation with the pBI-TPSS-Thio were assayed for 3-ketothiolase activity by minor modification of the assay described by Senior, P. J. and Dawes, E. A., Biochem. J. 134: 225-238, 1973. Frozen leaf tissues from kanamycin resistant heterozygote T1 plants were homogenized in Tris-buffer and the clarified crude extracts were tested for 3-ketothiolase activity. The results of these experiments are presented in Table 2.

Table 2.

Levels of 3-ketothiolase activity in transgenic *A. thaliana* plants.

sample	3-ketothiolase activity <sup>a</sup>
TPSS-Red	0.005
TPSS-Thio GH11	0.32
TPSS-Thio L	0.30
TPSS-Thio STU4	0.27

<sup>a</sup> Micromoles of acetoacetyl-CoA degraded per minute per milligram of protein. Values are an average of two to four measurements.

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Extracts of untransformed plants, transgenic plants transformed with pBI-TPSS-Red and transgenic plants transformed with pBI-TPSS-Thio which did not express the gene as detected by Western blot analysis had very low levels of 3-ketothiolase activity under the assay conditions. By contrast, each of the transgenic plants found to have a high 3-ketothiolase production in the Western blot analysis had also an increased level of 3-ketothiolase activity. This indicates that the modified bacterial 3-ketothiolase is functional in plants. The specific activity of the modified 3-ketothiolase was as active as the unmodified bacterial 3-ketothiolase expressed in the cytoplasm of *Arabidopsis* plants.

Transgenic plants obtained by transformation with the pBI-TPSS-Red were assayed for acetoacetyl-CoA reductase activity by minor modifications of the assay described by Senior, P. J. and Dawes, E. A., *Biochem. J.* 134: 225-238, 1973. Leaves from kanamycin resistant heterozygote T1 plants were homogenized in potassium phosphate buffer and the clarified extracts were assayed for acetoacetyl-CoA reductase activity. The results of these experiments are presented in Table 3.

Table 3.

Levels of acetoacetyl-CoA reductase activity in transgenic *A. thaliana* plants.

sample	acetoacetyl-CoA reductase activity <sup>a</sup>
TPSS-Syn	0.047
TPSS-Red DEF	1.13
TPSS-Red GHI1	0.49
TPSS-Red GHI2	0.75
TPSS-Red MNO1	1.07
TPSS-Red MNO2	0.31
TPSS-Red STU	3.39
TPSS-Red VWX	0.28

<sup>a</sup> Micromoles of NADPH oxidized per minute and milligram of protein. Values are an average of two to four measurements.

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Extracts from plants which were untransformed, transformed with pBI-TPSS-Thio or transformed plants which did not express the gene as detected by Western blot analysis had undetectable levels of acetoacetyl-CoA reductase. By contrast, each of the transgenic plants which were found to produce the acetoacetyl-CoA reductase in the Western blot analysis showed acetoacetyl-CoA reductase activity. The level of activity correlated with the level of production seen in the Western blot. This indicates that the modified bacterial acetoacetyl-CoA reductase is functional in plants.

Transgenic plants obtained by transformation with the construct pBI-TPSS-Syn were not assayed for the presence of PHB synthase activity because of technical difficulties in measuring the activity of this enzyme in the absence of thiolase and reductase activities (Peoples, O. P. and Sinskey, A. J., J. Biol. Chem. 264: 15298-15303, 1989).

In summary, the results of these experiments indicate that all three enzymes involved in PHB synthesis modified for plastid targeting were produced to significant levels in plants, were processed in the manner expected for transport to the plastid and were enzymatically active.

6.1.2. Analysis of putative transgenic plants obtained after transformation with pBIB-CCN-Thio, pBIB-KCN-Red and pBIB-HCN-Syn.

In order to determine whether the putative transgenic plants transformed with pBIB-CCN-Thio, pBIB-KCN-Red and pBIB-HCN-Syn produce the appropriate enzyme, the proteins in the immature seeds were analyzed. Since Pang et al. showed that the seed specific promoter used in these experiments directs a high gene expression between day 6 and day 14 after fertilization of the flowers, the seeds were collected in this period (Pang, P. P., Pruitt, R. E. and

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Meyerowitz, E. M., Plant Mol. Biol. 11: 805-820, 1988). Frozen immature seeds were homogenized in buffer and the proteins present in the aqueous phase were separated by SDS polyacrylamide gel electrophoresis. The proteins  
5 were transferred to nitrocellulose and incubated with antibodies as described above.

Both plants obtained after transformation with pBIB-CCN-Thio showed a high level of expression of the enzyme in the Western blot. The enzyme appeared as a  
10 quadruplet at sizes between 43 and 47 KDa. The band at 47 KDa represents the size expected for the correctly processed form of the modified enzyme (Figure 9).

In the Western blot analysis of the 6 kanamycin resistant plants only the protein extract of  
15 plant 17-3K reacted with the antibody raised against the acetoacetyl-CoA reductase. The signal appeared as a double band at the size of the correctly processed form of the protein (29 KDa) and a slightly larger protein (31 KDa) (Figure 10).

Thirteen of the 17 plants obtained after transformation with pBIB-HCN-Syn were analyzed. Among  
20 these, 11 plants showed low level expression of the modified bacterial synthase. The transgenic plant TPSS-Syn 34-1G1 has an approximately five times higher level of expression than the other transgenic plants. The  
25 signal appears as a single band of the size of the processed enzyme (63 KDa) (Figure 11).

The preliminary results of the modified PHB enzymes expressed under control of the seed-specific  
30 promoter indicate that they are being synthesized in the seeds and are processed in the manner expected for targeting to the plastid.

After obtaining the homozygote lines of the transformed plants expressing to a high level the  
35 appropriate *phb* enzymes, immuno localization studies will be undertaken to further show that the enzymes are located in the plastids.

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## 6. 2. Analysis of the integration of the *phb* genes in transgenic plants

In order to verify the proper integration of the *phb* genes in the various transgenic plant lines produced, the genomic DNA of the transgenic plants was analyzed. High molecular weight DNA from control untransformed plants and from T2 transgenic plants transformed with the plasmids pBI-TPSS-Thio, pBI-TPSS-Red and pBI-TPSS-Syn or pBIB-CCN-Thio, pBIB-KCN-Red and pBIB-HCN-Syn was isolated. The DNAs were digested with the restriction enzymes HindIII, the fragments separated by agarose gel electrophoresis and transferred onto a nylon filter. In the constructs pBI-TPSS-Thio, pBI-TPSS-Red and pBI-TPSS-Syn, the restriction enzyme HindIII cuts only once at the 5' end of the CaMV 35S promoter (Figure 4). In the construct pBIB-CCN-Thio, pBIB-KCN-Red and pBIB-HCN-Syn, the restriction enzyme HindIII cuts several times, but only 5' of the coding region of the *phb* genes. Fragments detected using *phb* gene specific probes should therefore represent junction fragments of the Ti vectors with the plant genomic DNA, or internal fragments of concatemeric Ti vectors. The inserts in plasmids pUC-THIO, pUC-RED and pUC-SYN were excised by treatment with EcoRI and HindIII, purified by electrophoresis and labeled with <sup>32</sup>P-deoxyribonucleotides by random priming. The labeled *phb* gene fragments were then used to probe the nylon filters. The filters were hybridized and subsequently washed under high stringency conditions. The result of these filter hybridizations is shown in Figure 12 for the pBI-TPSS-*phb* constructs and in Figure 13 for the pBIB-CN-*phb* constructs. None of the three *phb* genes can be detected in untransformed control plants (Figure 12 a, b, c and 13 a, b, c, lane C).

The *phbA* gene was detected in the three transgenic lines produced by transformation with the plasmid pBI-TPSS-Thio (Figure 12 a, lane Thio 1-3) and



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in the two transgenic lines produced by transformation with the plasmid pBIB-CCN-Thio (Figure 13 a, lane Thio 1-2).

5 The *phbB* gene was detected in the transgenic plants produced by transformation with the plasmid pBI-TPSS-Red (Figure 12 b, lanes Red 1-7) and in 2 of the six transgenic lines produced by transformation with the plasmid pBIB-KCN-Red (Figure 13 b, lane Red 1 and 5). Although the plant lines CN-Red 17-3, -17-1dA, 17-1dB and  
10 -17-2K were resistant to 50  $\mu$ g/ml of kanamycin, suggesting the integration of the NPTII gene, no *phbB* gene could be detected. It is likely that only the fragment of the Ti vector harboring the NPTII gene, and not the *phbB* gene, was integrated in the genomic DNA of  
15 these lines (Figure 13 b, lane Red 2, 3, 4, 6).

The *phbC* gene was detected in the four transgenic plant lines produced by transformation with pBI-TPSS-Syn (Figure 12 c, lane Syn 1-4) and in the six transgenic plants lines produced by transformation with  
20 the plasmid pBIB-HCN-TPSS-Syn, which were analysed (Figure 13 c, lane Syn 1-6). The transgenic plant lines CN-Syn 34-1bA and CN-Syn 34-1bB are identical since they have the same pattern of bands on the Southern blot (Figure 13 c, lane Syn 1 and 2). The same phenomenon  
25 can be seen for the plants CN-Syn 34-1Hb and CN-Syn 34-1G1 (Figure 13 c, lane Syn 3 and 4) and the plants CN-Syn 35-1 and CN-Syn 35-1a (Figure 13 c, lane Syn 5 and 6) and is related to the transformation method.

30 A series of sexual crosses was used to construct plant lines containing all three *phb* enzymes in the plastid of all tissues. Three transgenic lines expressing high amounts of acetoacetyl-CoA reductase in the plastid (lines TPSS-Red DEF, MNO1 and STU) were  
35 cross-pollinated with transgenic plants producing high amount of PHB synthase in the plastid (lines TPSS-Syn GHI1, GHI2 and VWX). The resulting hybrid

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TPSS-Red/TPSS-Syn plants expressing acetoacetyl-CoA reductase and PHB synthase in the plastid did not produce measurable amounts of PHB in expanding leaves, as analyzed by gas chromatography ( $<20 \mu\text{g/g}$  fresh weight PHB). By comparison, transgenic plants producing the acetoacetyl-CoA reductase and the PHB synthase to similar level in the cytoplasm produced PHB (Poirier, Y., Dennis, D.E., Klomparens, K., and Somerville, C.R. Science 256, 520-523, 1992 and patent application Serial No. 07/732,243). A possible reason for this difference is that plastids may not have sufficient 3-ketothiolase to support PHB production. This is consistent with evidence that the early steps of the mevalonate pathway leading from acetyl-CoA to isopentenyl-pyrophosphate are absent in differentiated plastids (Kreuz, K. & Kleinig, H. Eur. J. Biochem. 141, 531-535, 1984, Schultz, G. & Schulze-Siebert, D. in Biological Role of Plant Lipids, eds. Biacs P.A., Gruiz, K., & Kremmer, T. (Plenum Publishing Corporation, New York, NY) pp. 313-319, 1989).

In order to establish a complete PHB biosynthetic pathway in plastids of all tissues, transgenic *A. thaliana* having a high amount of thiolase (line TPSS-Thio L) were cross-pollinated with the TPSS-Red/TPSS-Syn hybrids. From five combinations of crosses, a number of hybrids were obtained producing PHB and having therefore all three enzymes necessary for PHB production (TPSS-Thio L/TPSS-Red DEF/TPSS-Syn GHI1, TPSS-Thio L/TPSS-Red STU/TPSS-Syn GHI1, TPSS-Thio L/TPSS-Red STU/TPSS-Syn-GHI2, TPSS-Thio L/TPSS-Red STU/TPSS-Syn VWX, TPSS-Thio L/TPSS-Red MNO1/TPSS-Syn VWX). Hybrids producing PHB were first identified by epifluorescence microscopy of tissues stained with Nile Blue A. Plants with high levels of fluorescence had higher levels of PHB than plants with comparatively lower levels of fluorescence. PHB produced in these hybrids was then quantified by gas chromatography and

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identified by GC-MS analysis (Figure 14, 15). The amount of PHB in expanding leaves of 20 to 30 day old plants ranged from 20  $\mu\text{g}$  of PHB/g fresh weight to 700  $\mu\text{g}$  of PHB/g fresh weight (Figure 16 A). The triple hybrids continued to accumulate PHB throughout the life of the plants so that in the leaves of senescing plants levels of PHB were 8 to 13 times higher than the amount in expanding leaves (i.e., up to 7 mg PHB/g fresh weight) (Figure 16 B). This increase in PHB accumulation with time was observed in plants with a low initial PHB content (100  $\mu\text{g/g}$  fresh weight in expanding leaves reaching 1.1 mg/g in pre-senescing leaves) as well as in plants with a high initial PHB content (700  $\mu\text{g/g}$  fresh weight in expanding leaves reaching 7 mg/g fresh weight in pre-senescing leaves). In a TPSS-Thio L/TPSS-Red DEF/TPSS-Syn GHI1 hybrid, the maximal amount of PHB measured in the senescing leaves was approximately 14% of their dry weight (10 mg/g fresh weight).

Plants producing PHB in the plastid showed wild type growth and fertility even at the highest level of PHB accumulation (Figure 17). No differences were observed with wild type in the rate of germination of seeds of hybrids producing high level of PHB. However, plants producing more than 300 - 400  $\mu\text{g}$  PHB/g fresh weight in expanding leaves could be distinguished from the wild type by visual inspection during the later stages of growth. In these plants, the leaves showed slight chlorosis after approximately 50 - 60 days of growth, indicating that at very high levels of PHB accumulation (>3 mg PHB/g fresh weight) some aspect of chloroplast metabolism may be affected (Figure 18).

Transmission electron microscopy of leaf samples of PHB- producing hybrids revealed that PHB accumulated as agglomerations of electron-lucent granules of approximately 0.2 to 0.7  $\mu\text{m}$ , surrounded by a thin layer of electron-dense material (Figure 19 A).

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Granules of similar appearance have been described for bacterial PHB (Lundgren, D.G., Pfister, R.M., & Merrick, J.M. J. Gen. Microbiol. 34, 441-446, 1964) or for PHB in the cytoplasm, nucleus and vacuole of plant cells (Poirier, Y., Dennis, D.E., Klomparens, K., and Somerville, C.R. Science 256, 520-523, 1992 and patent application Serial No. 07/732,243). In plants expressing the plastid targeted *phb* enzymes, these granule agglomerations were exclusively located in the plastids. This is in contrast with transgenic plants expressing the PHB biosynthetic pathway in the cytoplasm which accumulated PHB in the nucleus, vacuole and cytoplasm, but not in the plastid (Poirier, Y., Dennis, D.E., Klomparens, K., and Somerville, C.R. Science 256, 520-523, 1992 and patent application Serial No. 07/732,243). PHB granules were clearly distinguished from starch granules in form, appearance and organization of the granules as visualized by conventional electron-microscopy fixation protocol. PHB granules are small, round electron-translucent granules forming dense agglomerations (Figure 17a). In comparison, starch appears as singular, electron-denser granules of ovular form, surrounded by an diffuse area (Figure 19 B). In tri-hybrids producing only a low amount of PHB in expanding leaves, it appeared by electron microscopy analysis that not all chloroplasts accumulated PHB. The reason for this is not known. There were no indications for differential expression of the transgenes in different tissues. Conceivably, it could simply reflect the fact that electron microscopy analysis only allows inspection of a small area of the total plastid volume. It could also reflect the action of co-suppression which may lead to a mosaic of differential expression, as observed in *Petunia* (Jorgensen, R. Trends in Biotechnology 8, 340-344, 1990). In old leaves of tri-hybrids accumulating high levels of PHB, almost all chloroplasts contained PHB.

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In order to gain insights into the mechanisms responsible for the different amounts of PHB produced in the various hybrids, the level of the 3-ketothiolase and acetoacetyl-CoA reductase activity present in PHB producing plants was measured in clarified crude leaf protein extracts. The PHB synthase was analyzed by Western blot analysis. The 3-ketothiolase activity in TPSS-Thio L/TPSS-Red/TPSS-Syn hybrid plants ranged from 0.001 to 0.8 u/mg protein. In contrast, the 3-ketothiolase activity in the parental TPSS-Thio L plants was 0.84 +/-0.15 u/mg protein. Southern blot analysis of the TPSS-Thio L line revealed 4 bands which hybridized to the *phbA* gene, probably corresponding to several independent integrations of the construct (Figure 12A, TPSS-Thio lane 2). Therefore, segregation of the different pBI-TPSS-Thio constructs may have caused the range of 3-ketothiolase activities in the F1 generation. Such variation can be readily eliminated by using standard plant breeding methods to develop true breeding lines that are homozygous for the various transgenes of interest. The acetoacetyl-CoA reductase activity in TPSS-Thio L/TPSS-Red DEF/TPSS-Syn GHI1 hybrid plants ranged from 0.007 to 0.78 u/mg protein. The acetoacetyl-CoA reductase activity in the TPSS-Red DEF/TPSS-Syn GHI1 hybrid which served as a the parent in the cross with TPSS-Thio L was 2.09 +/- 0.23 u/mg protein. Southern blot analysis and analysis of the segregation ratio of the selectable marker in the F1 generation indicated that TPSS-Red DEF plants harbor the construct pBI-TPSS-Red at a single integration site (Figure 12b, TPSS-Red lane 1). Western blot analysis indicated that the reduced activity was correlated with an approximately 10-fold reduction in protein amount in the clarified extracts of PHB-producing plants. Similarly, PHB-producing hybrid plants TPSS-Thio L/TPSS-Red STU/TPSS-Syn GHI1, TPSS-Thio L/TPSS-Red STU/TPSS-Syn GHI2, TPSS-ThioL/TPSS-Red STU/TPSS-Syn VWX, and TPSS-

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Thio L/TPSS-Red MNO1/TPSS-Syn VWX also had widely varying and unexpectedly low reductase activities in comparison to their parent plants which was correlated with low amounts of protein in Western blot analysis.

5 The reason for the variable and unusually low amount of reductase activity in tri-hybrids cannot be explained by changes in the copy number of the pBI-TPSS-Red construct. This variability is though to be due to the fact that all transcripts of the modified *phb* genes  
10 contain a common sequence of 243 bp, namely the coding region of the transit peptide (TPSS) (Figure 3). Gaining one or more thiolase genes modified with the coding region of the TPSS might down regulate other TPSS containing genes, such as TPSS-Red, by the mechanism of  
15 co-suppression (Jorgensen, R. Trends in Biotechnology 8, 340-344, 1990, Seymour, G.B., Fray, G.R., Hill, P, & Tucker G.A. Plant Mol. Biol. 23, 1-9, 1993). Co-suppression may also provide an explanation of why, upon  
20 examination by transmission electron microscopy, some cells appeared to be full of PHB whereas adjoining cells showed no PHB. Therefore, in order to avoid co-suppression and alleviate the variable and low expression of the *phb* genes in plants producing PHB, all  
25 *phb* genes should be modified for plastid targeting by the addition of a different transit peptide for each of the introduced *phb* genes. Sequences are now available for dozens of different chloroplast-localized proteins including the sequences of their transit peptides. Therefore, methods for improvements of the current  
30 invention by the replacement of part or all of the amino terminal transit peptides used in this example with that of a normally chloroplast-localized protein will be evident to one skilled in the art.

35 The presence of PHB synthase was investigated by Western blot analysis of leaf protein extracts of PHB-producing plants. In TPSS-Thio/TPSS-Red/TPSS-Syn

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hybrid plants, PHB synthase could never be detected in the soluble protein fraction. However, PHB synthase was readily detectable on Western blot of solubilized membrane and particulate fractions of plant extracts. In contrast, in plants transformed only with the pBI-TPSS-Syn, PHB synthase could be detected in the soluble fraction (Figure 20). This finding suggests that the PHB synthase is closely associated with the PHB granules formed in plants as shown for the PHB synthase in bacteria (Fukui, T., Yoshimoto, A., Matsumoto, M., Hosokawa, S. Saito, T., Nishikawa, H., & Tomita, K. Arch. Microbiol. 110, 149-156, 1976, Haywood, G.W., Anderson, A.J. and Dawes E.A. FEMS Microbiol. Lett. 57, 1-6, 1989).

In general, transgenic plants with the highest levels of both 3-ketothiolase and acetoacetyl-CoA reductase activities had the highest levels of PHB and plants with low levels of both activities had the lowest levels of PHB. There was no obvious plateau in PHB production at the highest levels of measurable enzyme activity. Therefore, it appeared that PHB accumulation was limited by the amount of enzyme activity rather than by the availability of acetyl-CoA. Therefore, it should be possible to increase the amount of PHB produced in transgenic plants beyond the amount described in this patent application by increasing the amount of the various *phb* enzymes produced in plants. One way to achieve this is to avoid the phenomenon of co-suppression of modified *phb* genes possessing the same transit peptide (for targeting to the plastid) by using a different plastid targeting sequence for each of the *phb* genes introduced in plants. It may also be possible to increase the amount of *phb* enzymes produced in transgenic plants by using strong promoters leading to higher expression level than possible with the CaMV or CRB promoters used in these experiments. Because the codon usage of the bacterial coding sequences of the *phb*

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genes is not typical for higher plants, it should also be possible to increase expression of the enzymes by altering the coding sequence of the bacterial genes so that the amino acid sequence is encoded by codons which are most commonly utilized by the higher plant in which the genes are to be expressed.

In summary, plants engineered to express the PHB biosynthetic pathway in their plastids accumulate PHB to high amounts. By changing the location of PHB production from a cellular compartment with a low flux through acetyl-CoA (cytoplasm) to a compartment with a high flux through acetyl-CoA (plastid), the maximal level of PHB production was increased by up to 100-fold (from approximately 100  $\mu$ g per gram fresh weight for cytoplasmic expression, as described in Poirier, Y., Dennis, D.E., Klomparens, K., and Somerville, C.R. Science 256, 520-523, 1992 and patent application Serial No. 07/732,243, to up to approximately 10 mg per gram fresh weight for plastid expression, as described in the present application). Plants producing high levels of PHB in the plastids showed normal growth and vigor. This indicates that PHB is not toxic for plants and that there appears to be no biological barrier to PHB production in plastids. Depletion of metabolites from essential metabolic pathways of the cytoplasm appears to have been the reason for the deleterious effect of PHB production in plants expressing the PHB enzymes in the cytoplasm (Poirier, Y., Dennis, D.E., Klomparens, K., and Somerville, C.R. Science 256, 520-523, 1992 and patent application Serial No. 07/732,243). However, since PHB granules were also located in the nucleus, it might be possible that the interaction of the PHB granules with nuclear constituents was also a cause of the deleterious effect of PHB production in these plants.

A similar analysis will be performed with transgenic plants expressing the modified *phb* genes



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under the control of the seed-specific promoter CRB. Plants transformed with pBIB-KCN-Red, producing a substantial amount of acetoacetyl-CoA reductase in the plastid of developing seeds, will be cross-pollinated with plants transformed with pBIB-HCN-Syn, producing a substantial amount of PHB synthase in the plastid of developing seeds. The resulting hybrids will be analyzed for PHB production in the seeds by GC-MS analysis and electron microscopy. Since it is not obvious that the amount of endogenous acetoacetyl-CoA in the plastid of the developing seed is sufficient to allow PHB production, the 3-ketothiolase modified for plastid targeting in the plastid of developing seed will be introduced to create a tri-hybrid. In order to create a tri-hybrid producing all three enzymes, reductase/synthase double hybrids will be cross-pollinated with transgenic plants expressing the 3-ketothiolase in the plastid of developing seeds. The high amount of PHB produced in the seeds of the resulting thiolase/reductase/synthase tri-hybrids will be analyzed by GC-MS and electron microscopy.

This method for producing PHB in plastids is not restricted to the use of hybrid plants produced by crossing various transgenic lines. A preferred alternate implementation of the method would involve placing all three genes on a colinear DNA molecule for simultaneous introduction into the host plant. It is also envisioned that the general method for causing high levels of PHB production described herein are generally applicable method to all higher plants and that the minor modifications of the methods which may be required to introduce and cause expression of the genes, and transport of the proteins into the plastids in other species of higher plants will be evident to those skilled in the art.

## Materials and methods

### Construction of DNA Recombinants

*E.coli* strain DH5 $\alpha$  harboring plasmids were grown in LB broth supplemented with kanamycin (50  $\mu$ g/ml) or ampicillin (50  $\mu$ /ml). Preparations of plasmid DNA was done by the alkaline lysis procedure of as described by Sambrook, J., Fritsch, E. F. and Maniatis, T. Molecular cloning: a laboratory manual, Cold Spring Harbor Laboratory Press (1989) and if necessary a purification with the magic mini DNA affinity columns (Promega Corp., WI). Plasmid DNA was cleaved with restriction endonucleases according to the manufacturers recommendations (New England Biolabs, Mass; Promega Corp., WI; Boehringer Mannheim Biochemicals, IN; Stratagene, CA), separated by agarose gel electrophoresis and visualized by ethidium bromide staining as described by Sambrook, J., Fritsch, E. F. and Maniatis, T. Molecular cloning: a laboratory manual, Cold Spring Harbor Laboratory Press (1989). The DNA fragments were recovered from the agarose gel by a freeze throw method and phenol extractions. Briefly, the agarose fragment is sliced into very small pieces with a razor blade, the same volume of phenol (prepared as described in Sambrook, J., Fritsch, E. F. and Maniatis, T. Molecular cloning: a laboratory manual, Cold Spring Harbor Laboratory Press (1989)) is added and vigorously vortexed. The suspension is twice frozen and thrown and subsequently centrifuged. The fragment containing supernatant is furthermore purified by Phenol-chloroform extractions and ethanol precipitation. In some experiments, the recessed 3' termini of DNA fragments were converted into blunt ends with T4 DNA polymerase using the protocol described in Sambrook, J., Fritsch, E. F. and Maniatis, T. Molecular cloning: a laboratory manual, Cold Spring Harbor Laboratory Press (1989). Ligation of DNA fragments with cohesive or blunt ends was done at 14°C for 16 h in buffer

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containing 50 mM Tris-HCl (pH 7.6), 5 mM MgCl<sub>2</sub>, 5% (w/v) polyethylene glycol 8000, 0.5 mM ATP and 5 mM dithiothreitol as described by Sambrook, J., Fritsch, E. F. and Maniatis, T. Molecular cloning: a laboratory manual, Cold Spring Harbor Laboratory Press (1989). A fraction of the ligation reaction was transferred into *E. coli* by the rubidium chloride method as described by Hanahan, D., J. Mol. Biol. 166:557-580 (1983). The transformed bacteria were plated on agar plates containing LB broth and either 50 µg/ml kanamycin or 50 µg/ml ampicillin. Preparation of radiolabeled DNA probes and hybridization are described in a following section.

Oligonucleotides were synthesized by the biochemistry facility at Michigan State University.

Polymerase chain reaction (PCR) was performed using a Perkin-Elmer Cetus DNA thermal cycler (Perkin-Elmer, CT). The reaction mixture contained 200 pmoles of 2 oligonucleotides PCR primers (Table 1), 200 ng of plasmid (table 1), and 2.5 units of Vent polymerase in buffer conditions recommended by the supplier (New England Biolabs Inc, Mass.). The DNA thermal cycler program for the amplifications of the bacterial PHB enzymes was as follow: 4 min at 95°C, 30 cycles of the sequence 1.5 min at 97°C - 2 min at 65°C - 3 min at 72°C, and finally 7 min at 72°C. For the TPSS fragment: 4 min at 95°C, 30 cycles of the sequence 1.5 min at 95°C - 2 min at 60°C - 2 min at 72°C, and finally 7 min at 72°C and for the CRB promoter: 4 min at 95°C, 30 cycles of the sequence 1.5 min at 95°C - 2 min at 58°C - 2 min at 72°C, and finally 7 min at 72°C. The PCR products was isolated by agarose gel electrophoresis and purified as described above.

Extraction and Restriction Endonuclease Cleavage of Genomic DNA

Wild type and transgenic plants were grown in

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soil for 2-3 weeks and approximately 5 g of leaf material was collected and frozen in liquid nitrogen. High molecular weight DNA was extracted from the frozen plant tissues as described by Rogers, S. C. and Bendich, A. J., Plant Molecular Biology Manual A6: 1-10 (1988). Restriction endonuclease cleavage with the enzyme HindIII on 1  $\mu$ g of DNA was performed under the conditions recommended by the manufacturer (New England Biolabs Inc, Mass.).

#### Agarose Gel Electrophoresis and Hybridization Procedure

DNA analysis by agarose gel electrophoresis and transfer to nylon membranes (Hybond-N, Amersham, Il.) were done using established procedures described by Southern et al. (1975) and Sambrook, J., Fritsch, E. F. and Maniatis, T. Molecular cloning: a laboratory manual, Cold Spring Harbor Laboratory Press (1989). Specific cloned DNA fragments to be used as probes were excised from the vector with appropriate restriction endonucleases, the inserts were purified from the vector by agarose gel electrophoresis and electroelution. Fragments were labeled with  $^{32}$ P-deoxyribonucleotides by the random primer extension method using hexamers as described by Feinberg, A. P. and Vogelstein, B., Anal. Biochem. 132, 6-13 (1983). Nylon filters were hybridized with labeled probes and exposed on film as described by Poirier, Y. and Jolicoeur, P., J. Virol. 63, 2088-2098 (1989).

#### Construction of Fusion proteins and Raising of Antibodies

For raising antibodies against the 3-ketothiolase, acetoacetyl-CoA reductase and PHB synthase of *A. eutrophus* fusionproteins with the maltose binding protein *malE* of *E. coli* were constructed by using the pIH821 vector (New England Biolabs Inc, Mass.).

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The MALE-Thiolase fusionprotein was constructed by purifying the 1.2 kbp XhoII-EcoRI fragment of the pUC-Thio plasmid (Somerville, C. R., Poirier, Y., and Dennis, D. E., patent application serial no. 07/732,243), filling in the ends by T4-DNA polymerase and cloning it in pIH821. The vector had been prepared by digestion with XbaI and filling in the end by T4-DNA polymerase. Clones carrying the insert in the desired orientation contain the gene fusion in a way that the reading frame is correct to obtain the MALE-Thiolase fusion. The plasmid was designated as *pmalE*-Thio.

To obtain the MALE-Reductase fusionprotein the pUC-Red plasmid (Somerville, C. R., Poirier, Y., and Dennis, D. E., patent application Serial No. 07/732,243) was digested with DdeI and SacI. After purification of the 0.7 kbp fragment, the ends were filled in with T4-DNA polymerase. The blunt ended fragment was cloned in the XbaI digested and blunt ended pIH821 vector as described above. The clone containing the fragment in the exact orientation for expression of the MALE-Reductase expression was designated as *pmalE*-Red.

For the construction of the MALE-Synthase fusion protein the pUC-Syn was digested with NcoI and the ends were filled with T4-DNA polymerase. Subsequently, the plasmid was digested with HindIII and the 1.6 kbp fragment was cloned into the pIH821. The vector had been prepared by digesting with XbaI and filling in the end with T4 DNA Polymerase and subsequently digesting with HindIII. The clones were designated as *pmalE*-Syn.

The *pmalE*-Thio, -Red and -Syn plasmids were transformed into DH5 $\alpha$  and the fusion proteins were expressed and purified as described by the manufacturer (New England Biolabs Inc, Mass). The fusion proteins were injected into rabbits to raise polyclonal antibodies by using Freund's adjuvants as immunostimulants.

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## Assay for 3-Ketothiolase Activity

Frozen leaf samples (0.1 g) were homogenized in 200  $\mu$ l of ice-cold thiolase buffer containing 100 mM Tris-HCl (pH 8.0), 40 mM  $MgCl_2$  and 5 mM  $\beta$ -mercaptoethanol. The homogenate was clarified by centrifugation at 10000 x g for 5 min and the supernatant transferred to a fresh tube. The protein content of the extract was measured by the Bradford assay using the Bio Rad protein assay kit (Bio Rad Laboratories, CA). Between 3 to 30  $\mu$ g of plant protein extract was used per assay. Activity of the 3-ketothiolase enzyme in the different extracts was assayed according to the procedure of Senior, P. J. and Dawes, E. A., Biochem. J. 134: 225-238, 1973.

## Assay for Acetoacetyl-CoA Reductase Activity

Frozen leaf samples (0.1 g) were homogenized in 200  $\mu$ l of ice-cold reductase buffer containing 100 mM  $KH_2PO_4$  (pH 5.5), 0.02 mM  $MgCl_2$  and 4.0 mM  $\beta$ -mercaptoethanol. The homogenate was clarified by centrifugation at 10000 x g for 5 min and the supernatant transferred to a fresh tube. The protein content of the extract was measured by the Bradford assay using the Bio Rad protein assay kit. Between 0.8 to 10  $\mu$ g of plant protein extract was used per assay. Activity of the acetoacetyl-CoA reductase enzyme was assayed according to the procedure of Senior, P. J. and Dawes, E. A., Biochem. J. 134: 225-238, 1973.

## Western Blot Analysis

For Western blot analysis, crude protein extracts prepared as described above for the enzyme activity assays were used. For the analysis of the expression of PHB synthase frozen leaf samples (0.1 g) were homogenized in 200  $\mu$ l ice-cold buffer containing 100 mM Tris-HCl (pH 8.0), 5 mM EDTA and 4 mM  $\beta$ -mercaptoethanol. The homogenate was clarified by

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centrifugation at 10000 x g for 5 min and the supernatant transferred to a fresh tube. In some experiments, the membrane and particulate fractions were partly solubilized in extraction buffer containing 1% SDS and again clarified by centrifugation. The protein content of these samples was measured by a modified Lowry method (Markwell, M.A.K., Haas, M., Bieber, L.L. and Tolbert, N.E., Anal. Biochemistry 87, 206-210 (1978)).

10

Aliquots of the supernatants were separated by sodium dodecyl sulphate polyacrylamide gel electrophoresis (SDS PAGE) according to Laemmli, Nature 227: 680-685, 1970. The proteins were electrophoretically transferred to nitrocellulose filters. The Western blot analysis was performed as recommended in the ECL Western blotting protocol (Amersham International pIc, Amersham UK). For blocking the filters TBS (20 mM Tris-HCL, pH 7.6, 137 mM NaCl) with 5% fat-free milk powder/0.12% Tween 20 was chosen. The first antibody was diluted 1:1000 in blocking solution before incubating the filters. The antibody reaction was detected by the ECL Western blotting detection system (Amersham International pIc, Amersham UK).

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#### Analysis of polyhydroxybutyrate

For gas chromatographic analyses, 20-100 mg of leaf material was extracted 3-4 times with 50% ethanol and then with 100% methanol for 45 min - 1 h at 55 °C. Dry residues were extracted at 55°C with 0.5 ml chloroform for at least 12 h and transesterified for 4 - 6 h in 0.8 M HCl in ethanol at 100°C. After extraction with 0.9 M NaCl, the chloroform phase was analyzed on a Hewlett Packard 5890 series II gas chromatograph. Bacterial PHB (Sigma) was used as a standard. For visualization of PHB granules by epi-fluorescence microscopy, leaf samples were fixed in 2% glutaraldehyde

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in 10 mM phosphate buffer (pH 7.2) for 2 h. Tissues were rinsed in water and stained for 5 min in 1% Nile Blue A. Tissues were rinsed several times in water and soaked 1 min in 8% acetic acid followed by a final rinse of water. PHB granules were visualized by epifluorescence microscopy under an excitation wavelength of 546 or 565 nm (Ostle, A.G. & Holt J.G. Appl. Environ. Microbiol. 44, 238-241, 1982).

10 Transmission-electron microscopy.

Tissues samples were fixed in 0.8% glutaraldehyde/2% paraformaldehyde in 0.01 M phosphate buffer (pH 7.2) for 2 h under a slight vacuum. After 4 washes with phosphate buffer, the samples were treated with 1% osmium tetroxide for 40 to 60 min. The samples were dehydrated in a graded ethanol series and embedded in Spurr's resin (Ted Pella Inc.). Sections of 80-90 nm were cut, placed on copper grids, and stained with 5% uranyl acetate for 30-45 min, following by staining with Reynolds lead citrate for 3-4 min. Sections were viewed in a JEOL100CX II transmission electron microscope operated at 80 kV.

Although the specific example of the invention described here involved the plant *Arabidopsis thaliana*, genes from *Alcaligenes eutrophus* and a transit peptide of pea, the invention is of general utility. The claims pertaining to production of poly-D-(-)-3-hydroxybutyrate and/or polyhydroxyalkanoate in the plastids of plants is not limited to *Arabidopsis thaliana*, or linked specifically to the use of genes from *Alcaligenes eutrophus* or the described transit peptide for plastid targeting. The claims described below describe a general method for the production of polyhydroxyalkanoate in the plastid of plants through the introduction of foreign DNA material into plant cells.



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The improvements in the present invention are:

1-Transformation of plant cells with foreign DNA material encoding information leading to the production in the plastid of an enzyme possessing a 3-ketothiolase activity. The term "foreign DNA material" refers to DNA material which is not normally present in an organism, but which is introduced into a cell and resides either integrated into the chromosome, or resides in an extra-chromosomal form. An increase in 3-ketothiolase activity in the plastids of plant cells results from the introduction of foreign DNA material into plant cells.

2-Transformation of plant cells with foreign DNA material encoding information leading to the production in the plastids of an enzyme possessing an acetoacetyl-CoA reductase activity. An increase in acetoacetyl-CoA reductase activity in the plastids results from the introduction of foreign DNA material into plant cells.

3-Transformation of plant cells with foreign DNA material leading to the production of hydroxyacyl-CoA in the plastids which is foreign to the plant cell. Transformation of plant cells with foreign DNA material leading to the production of an increased level of hydroxyacyl-CoA in the plastids of plant cells.

4-Transformation of plant cells with foreign DNA material encoding information leading to the production in the plastids of an enzyme possessing the ability to polymerize hydroxyacyl-CoA of plant cells. An increase in an enzyme activity leading to the polymerization of hydroxyacyl-CoA in the plastids of plant cells results from the introduction of foreign DNA material into plant cells.

5-Production of a polyhydroxyalkanoate, including poly-D-(-)-3-hydroxybutyrate, in the plastids of plant cells

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through the introduction of foreign DNA material into plant cells.

5 6-Production of polyhydroxyalkanoate in the plastids of plant cells, is preferably at a level higher than 2  $\mu$ g polyhydroxyalkanoate per gram of fresh plant material.

10 7-Production of polyhydroxyalkanoate in plastids is preferably at a level higher than 2  $\mu$ g polyhydroxyalkanoate per gram of fresh plant material, in any plant cell for which it is possible to introduce foreign DNA material.

15 8-Production of polyhydroxyalkanoate in the plastids of hybrid plants is preferably at a level higher than 2  $\mu$ g polyhydroxyalkanoate per gram of fresh plant material, resulting from cross-pollination between two parental plant lines having been transformed with foreign DNA material, but which by themselves do not produce  
20 polyhydroxyalkanoate in plastids, or produce polyhydroxyalkanoate at a level lower than produced in the hybrid plant.

25 9-Production of polyhydroxyalkanoate in the form of granules inside of the plastids of plant cells.

The seeds containing the genes of Figures 3 and 4 are maintained at Michigan State University, East Lansing, Michigan.

30 It is intended that the foregoing description be only illustrative of the present invention and that the present invention be limited only by the hereinafter appended claims.

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## APPENDIX I

## (1) GENERAL INFORMATION:

- (i) Applicant: Christopher R. Somerville,  
Christiane Nawrath,  
Yves Poirier
- (ii) Title of Invention: Processes For Producing  
Polyhydroxybutyrate and Related  
Polyhydroxyalkanoates in the Plastids of  
Higher Plants
- (iii) Number of Sequences: 3
- (iv) Correspondence Address:
  - (A) Addressee: Ian C. McLeod
  - (B) Street: 2190 Commons Parkway
  - (C) City: Okemos
  - (D) State: Michigan
  - (E) Country: USA
  - (F) Zip: 48864
- (v) Computer Readable Form:
  - (A) Medium Type: Diskette 5.25 inch, 360 kb storage
  - (B) Computer: Acer
  - (C) Operating System: MS-DOS (version 3.3)
  - (D) Software: Wordperfect 5.1
- (vi) Current Application Data:
  - (A) Application Number:
  - (B) Filing Date:
  - (C) Classification:
- (vii) Prior Application Data:
  - (A) Application Number: 08/108,193 and 07/732,243
  - (B) Filing Date: August 17, 1993 and July 19, 1991
- (viii) Attorney/Agent Information:
  - (A) Name: Ian C. McLeod
  - (B) Registration No.: 20,931
  - (C) Reference/Docket Number: MSU 4.1-222
- (ix) Telecommunication Information:
  - (A) Telephone: (517) 347-4100
  - (B) Telefax: (517) 347-4103

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## (2) Information for SEQ ID NO: 1

## (i) Sequence Characteristics:

(A) Length: 1431 Base Pairs

(B) Type: Nucleic Acid

(C) Strandedness: Double

(D) Topology: Linear

## (ii) Molecule Type:

(A) Description: Genomic DNA

## (iii) HYPOTHETICAL: No

## (iv) ANTI-SENSE: No

## (vi) ORIGINAL SOURCE:

(A) Organism: *Alcaligenes eutrophus*

## (vii) IMMEDIATE SOURCE:

(A) Library: Genomic

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1

ATG GCT TCT ATG ATA TCC TCT TCC GCT GTG ACA ACA GTC AGC CGT GCC TCT AGG	54
Met Ala Ser Met Ile Ser Ser Ser Ala Val Thr Thr Val Ser Arg Ala Ser Arg	
5 10 15	
GGG CAA TCC GCC GCA GTG GCT CCA TTC GGC GGC CTC AAA TCC ATG ACT GGA TTC	108
Gly Gln Ser Ala Ala Val Ala Pro Phe Gly Gly Leu Lys Ser Met Thr Gly Phe	
20 25 30 35	
CCA GTG AAG AAG GTC AAC ACT GAC ATT ACT TCC ATT ACA AGC AAT GGT GGA AGA	162
Pro Val Lys Lys Val Asn Thr Asp Ile Thr Ser Ile Thr Ser Asn Gly Gly Arg	
40 45 50	
GTA AAG TGC ATG CAG GTG TGG CCT CCA ATT GGA AAG AAG AAG TTT GAG ACT CTT	216
Val Lys Cys Met Gln Val Trp Pro Pro Ile Gly Lys Lys Lys Phe Glu Thr Leu	
55 60 65 70	
TCC TAT TTG CCA CCA TTG ACG AGA GAT TCC CGG GTG ACT GAC GTT GTC ATC GTA	270
Ser Tyr Leu Pro Pro Leu Thr Arg Asp Ser Arg Val Thr Asp Val Val Ile Val	
75 80 85 90	
TCC GCC GCC CGC ACC GCG GTC GGC AAG TTT GGC GGC TCG CTG GCC AAG ATC CCG	324
Ser Ala Ala Arg Thr Ala Val Gly Lys Phe Gly Gly Ser Leu Ala Lys Ile Pro	
95 100 105	
GCA CCG GAA CTG GGT GCC GTG GTC ATC AAG GCC GCG CTG GAG CGC GCC GGC GTC	378
Ala Pro Glu Leu Gly Ala Val Val Ile Lys Ala Ala Leu Glu Arg Ala Gly Val	
110 115 120 125	
AAG CCG GAG CAG GTG AGC GAA GTC ATC ATG GGC CAG GTG CTG ACC GCC GGT TCG	432
Lys Pro Glu Gln Val Ser Glu Val Ile Met Gly Gln Val Leu Thr Ala Gly Ser	
130 135 140	
GGC CAG AAC CCC GCA CGC CAG GCC GCG ATC AAG GCC GGC CTC GGC GCG ATG GTG	486
Gly Gln Asn Pro Ala Arg Gln Ala Ala Ile Lys Ala Gly Leu Gly Ala Met Val	
145 150 155 160	
CCG GCC ATG ACC ATC AAC AAG GTG TGC GGC TCG GGC CTG AAG GCC GTG ATG CTG	540
Pro Ala Met Thr Ile Asn Lys Val Cys Gly Ser Gly Leu Lys Ala Val Met Leu	
165 170 175 180	

GCC Ala	ACC Ala	ATC Ala	ATC Ala	ATG Ile	ATG Met	GCG Ala	GCG Gly	GAC Asp	GCC Ala	GAG Glu	GAG Ile	GTG Val	GTG Val	GCC Ala	GCC Gly	GCC Gly	CAG Gln	594			
185																		190	195		
GAA Glu	AAC Asn	ATG Met	AGC Ser	GCC Ala	GCC Ala	CCG Pro	CAC His	GTG Val	CTG Leu	CCG Pro	GGC Gly	TCG Ser	CGC Arg	GAT Asp	GGT Gly	TTC Phe	CGC Arg	648			
200																		205	210	215	
ATG Met	GGC Gly	GAT Asp	GCC Ala	AAG Lys	CTG Leu	GTC Val	GAC Asp	ACC Thr	ATG Met	ATC Ile	GTC Val	GAC Asp	GGC Gly	CTG Leu	TGG Trp	GAC Asp	GTG Val	702			
220																		225	230		
TAC Tyr	AAC Asn	CAG Gln	TAC Tyr	CAC His	ATG Met	GGC Gly	ATC Ile	ACC Thr	GCC Ala	GAG Glu	AAC Asn	GTG Val	GCC Ala	AAG Lys	GAA Glu	TAC Tyr	GGC Gly	756			
235																		240	245	250	
ATC Ile	ACA Thr	CGC Arg	GAG Glu	GCG Ala	CAG Gln	GAT Asp	GAG Glu	TTC Phe	GCC Ala	GTC Val	GGC Gly	TCG Ser	CAG Gln	AAC Asn	AAG Lys	GCC Ala	GAA Glu	810			
255																		260	265		
GCC Ala	GCG Ala	CAG Gln	AAG Lys	GCC Ala	GGC Gly	AAG Lys	TTT Phe	GAC Asp	GAA Glu	GAG Glu	ATC Ile	GTC Val	CCG Pro	GTG Val	CTG Leu	ATC Ile	CCG Pro	864			
275																		280	285		
CAG Gln	CGC Arg	AAG Lys	GGC Gly	GAC Asp	CCG Pro	GTG Val	GCC Ala	TTC Phe	AAG Lys	ACC Thr	GAC Asp	GAG Glu	TTC Phe	GTG Val	CGC Arg	CAG Gln	GGC Gly	918			
290																		295	300	305	
GCC Ala	ACG Thr	CTG Leu	GAC Asp	AGC Ser	ATG Met	TCC Ser	GGC Gly	CTC Leu	AAG Lys	CCC Pro	GCC Ala	TTC Phe	GAC Asp	AAG Lys	GCC Ala	GGC Gly	ACG Thr	972			
310																		315	320		
GTG Val	ACC Thr	GCG Ala	GCC Ala	AAC Asn	GCC Ala	TCG Ser	GGC Gly	CTG Leu	AAC Asn	GAC Asp	GGC Gly	GCC Ala	GCC Ala	GCG Ala	GTG Val	GTG Val	GTG Val	1026			
325																		330	335	340	
ATG Met	TCG Ser	GCG Ala	GCC Ala	AAG Lys	GCC Ala	AAG Lys	GAA Glu	CTG Leu	GGC Gly	CTG Leu	ACC Thr	CCG Pro	CTG Leu	GCC Ala	ACG Thr	ATC Ile	AAG Lys	1080			
345																		350	355	360	
AGC Ser	TAT Tyr	GCC Ala	AAC Asn	GCC Ala	GGT Gly	GTC Val	GAT Asp	CCC Pro	AAG Lys	GTG Val	ATG Met	GGC Gly	ATG Met	GGC Gly	CCG Pro	GTG Val	CCG Pro	1134			
365																		370	375		
GCC Ala	TCC Ser	AAG Lys	CGC Arg	GCC Ala	CTG Leu	TCG Ser	CGC Arg	GCC Ala	GAG Glu	TGG Trp	ACC Thr	CCG Pro	CAA Gln	GAC Asp	CTG Leu	GAC Asp	CTG Leu	1188			
380																		385	390	395	
ATG Met	GAG Glu	ATC Ile	AAC Asn	GAG Glu	GCC Ala	TTT Phe	GCC Ala	GCG Ala	CAG Gln	GCG Ala	CTG Leu	GCG Ala	GTG Val	CAC His	CAG Gln	CAG Gln	ATG Met	1242			
400																		405	410		
GGC Gly	TGG Trp	GAC Asp	ACC Thr	TCC Ser	AAG Lys	GTC Val	AAT Asn	GTG Val	AAC Asn	GGC Gly	GGC Gly	GCC Ala	ATC Ile	GCC Ala	ATC Ile	GGC Gly	CAC His	1296			
415																		420	425	430	
CCG Pro	ATC Ile	GGC Gly	GCG Ala	TCG Ser	GGC Gly	TGC Cys	CGT Arg	ATC Ile	CTG Leu	GTG Val	ACG Thr	CTG Leu	CTG Leu	CAC His	GAG Glu	ATG Met	AAG Lys	1350			
435																		440	445	450	
CGC Arg	CGT Arg	GAC Asp	GCG Ala	AAG Lys	AAG Lys	GGC Gly	CTG Leu	GCC Ala	TCG Ser	CTG Leu	TGC Cys	ATC Ile	GGC Gly	GGC Gly	GGC Gly	ATG Met	GGC Gly	1404			
455																		460	465		
GTG Val	GCG Ala	CTG Leu	GCA Ala	GTC Val	GAG Glu	CGC Arg	AAA Lys	TAA ***										1431			
470																		475			

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## (3) Information for SEQ ID NO: 2

## (i) Sequence Characteristics:

(A) Length: 990 Base Pairs

(B) Type: Nucleic Acid

(C) Strandedness: Double

(D) Topology: Linear

## (ii) Molecule Type:

(A) Description: Genomic DNA

## (iii) HYPOTHETICAL: No

## (iv) ANTI-SENSE: No

## (vi) ORIGINAL SOURCE:

(A) Organism: *Alcaligenes eutrophus*

## (vii) IMMEDIATE SOURCE:

(A) Library: Genomic

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATG	GCT	TCT	ATG	ATA	TCC	TCT	TCC	GCT	GTG	ACA	ACA	GTC	AGC	CGT	GCC	TCT	AGG	54
Met	Ala	Ser	Met	Ile	Ser	Ser	Ser	Ala	Val	Thr	Thr	Val	Ser	Arg	Ala	Ser	Arg	
				5					10					15				
GGG	CAA	TCC	GCC	GCA	GTG	GCT	CCA	TTC	GGC	GGC	CTC	AAA	TCC	ATG	ACT	GGA	TTC	108
Gly	Gln	Ser	Ala	Ala	Val	Ala	Pro	Phe	Gly	Gly	Leu	Lys	Ser	Met	Thr	Gly	Phe	
	20				25				30						35			
CCA	GTG	AAG	AAG	GTC	AAC	ACT	GAC	ATT	ACT	TCC	ATT	ACA	AGC	AAT	GGT	GGA	AGA	162
Pro	Val	Lys	Lys	Val	Asn	Thr	Asp	Ile	Thr	Ser	Ile	Thr	Ser	Asn	Gly	Gly	Arg	
			40				45						50					
GTA	AAG	TGC	ATG	CAG	GTG	TGG	CCT	CCA	ATT	GGA	AAG	AAG	AAG	TTT	GAG	ACT	CTT	216
Val	Lys	Cys	Met	Gln	Val	Trp	Pro	Pro	Ile	Gly	Lys	Lys	Lys	Phe	Glu	Thr	Leu	
	55			60					65					70				
TCC	TAT	TTG	CCA	CCA	TTG	ACG	AGA	GAT	TCC	CGG	GTG	ACT	CAG	CGC	ATT	GCG	TAT	270
Ser	Tyr	Leu	Pro	Pro	Leu	Thr	Arg	Asp	Ser	Arg	Val	Thr	Gln	Arg	Ile	Ala	Tyr	
	75				80							85			90			
GTG	ACC	GGC	GGC	ATG	GGT	GGT	ATC	GGA	ACC	GCC	ATT	TGC	CAG	CGG	CTG	GCC	AAG	324
Val	Thr	Gly	Gly	Met	Gly	Gly	Ile	Gly	Thr	Ala	Ile	Cys	Gln	Arg	Leu	Ala	Lys	
			95					100					105					
GAT	GGC	TTT	CGT	GTG	GTG	GCC	GGT	TGC	GGC	CCC	AAC	TCG	CCG	CGC	CGC	GAA	AAG	378
Asp	Gly	Phe	Arg	Val	Val	Ala	Gly	Cys	Gly	Pro	Asn	Ser	Pro	Arg	Arg	Glu	Lys	
	110				115					120					125			
TGG	CTG	GAG	CAG	CAG	AAG	GCC	CTG	GGC	TTC	GAT	TTC	ATT	GCC	TCG	GAA	GGC	AAT	432
Trp	Leu	Glu	Gln	Gln	Lys	Ala	Leu	Gly	Phe	Asp	Phe	Ile	Ala	Ser	Glu	Gly	Asn	
			130				135					140						
GTG	GCT	GAC	TGG	GAC	TCG	ACC	AAG	ACC	GCA	TTC	GAC	AAG	GTC	AAG	TCC	GAG	GTC	486
Val	Ala	Asp	Trp	Asp	Ser	Thr	Lys	Thr	Ala	Phe	Asp	Lys	Val	Lys	Ser	Glu	Val	
	145				150				155					160				

[illegible]

(4) Information for SEQ ID NO: 3

(i) **Sequence Characteristics:**

(A) Length: 2019 Base Pairs

(B) Type: Nucleic Acid

(C) Strandedness: Double

(D) Topology: Linear

(ii) Molecule Type:

(A) Description: Genomic DNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(vi) ORIGINAL SOURCE:

(A) Organism: *Alcaligenes eutrophus*

(vii) IMMEDIATE SOURCE:

(A) Library: Genomic

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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ATG	GCT	TCT	ATG	ATA	TCC	TCT	TCC	GCT	GTG	ACA	ACA	GTC	AGC	CGT	GCC	TCT	AGG	54
Met	Ala	Ser	Met	Ile	Ser	Ser	Ser	Ala	Val	Thr	Thr	Val	Ser	Arg	Ala	Ser	Arg	
				5					10					15				
GGG	CAA	TCC	GCC	GCA	GTG	GCT	CCA	TTC	GGC	GGC	CTC	AAA	TCC	ATG	ACT	GGA	TTC	108
Gly	Gln	Ser	Ala	Ala	Val	Ala	Pro	Phe	Gly	Gly	Leu	Lys	Ser	Met	Thr	Gly	Phe	
	20					25					30					35		
CCA	GTG	AAG	AAG	GTC	AAC	ACT	GAC	ATT	ACT	TCC	ATT	ACA	AGC	AAT	GGT	GGA	AGA	162
Pro	Val	Lys	Lys	Val	Asn	Thr	Asp	Ile	Thr	Ser	Ile	Thr	Ser	Asn	Gly	Gly	Arg	
			40				45						50					
GTA	AAG	TGC	ATG	CAG	GTG	TGG	CCT	CCA	ATT	GGA	AAG	AAG	AAG	TTT	GAG	ACT	CTT	216
Val	Lys	Cys	Met	Gln	Val	Trp	Pro	Pro	Ile	Gly	Lys	Lys	Lys	Phe	Glu	Thr	Leu	
					60					65					70			
TCC	TAT	TTG	CCA	CCA	TTG	ACG	AGA	GAT	TCC	CGG	GTG	GCG	ACC	GCG	AAA	GGC	GCG	270
Ser	Tyr	Leu	Pro	Pro	Leu	Thr	Arg	Asp	Ser	Arg	Val	Ala	Thr	Gly	Lys	Gly	Ala	
		75					80					85					90	
GCA	GCT	TCC	ACG	CAG	GAA	GGC	AAG	TCC	CAA	CCA	TTC	AAG	GTC	ACG	CCG	GGG	CCA	324
Ala	Ala	Ser	Thr	Gln	Glu	Gly	Lys	Ser	Gln	Pro	Phe	Lys	Val	Thr	Pro	Gly	Pro	
				95					100					105				
TTC	GAT	CCA	GCC	ACA	TGG	CTG	GAA	TGG	TCC	CGC	CAG	TGG	CAG	GGC	ACT	GAA	GGC	378
Phe	Asp	Pro	Ala	Thr	Trp	Leu	Glu	Trp	Ser	Arg	Gln	Trp	Gln	Gly	Thr	Glu	Gly	
	110					115					120					125		
AAC	GGC	CAC	GCG	GCC	GCG	TCC	GGC	ATT	CCG	GGC	CTG	GAT	GCG	CTG	GCA	GGC	GTC	432
Asn	Gly	His	Ala	Ala	Ala	Ser	Gly	Ile	Pro	Gly	Leu	Asp	GCG	Ala	Leu	Gly	Val	
			130					135					140					
AAG	ATC	GCG	CCG	GCG	CAG	CTG	GGT	GAT	ATC	CAG	CAG	CGC	TAC	ATG	AAG	GAC	TTC	486
Lys	Ile	Ala	Pro	Ala	Gln	Leu	Gly	Asp	Ile	Gln	Gln	Arg	Tyr	Met	Lys	Asp	Phe	
	145				150					155					160			
TCA	GCG	CTG	TGG	CAG	GCC	ATG	GCC	GAG	GGC	AAG	GCC	GAG	GCC	ACC	GGT	CCG	CTG	540
Ser	Ala	Leu	Trp	Gln	Ala	Met	Ala	Glu	Gly	Lys	Ala	Glu	Ala	Thr	Gly	Pro	Leu	
		165				170						175					180	
CAC	GAC	CGG	CGC	TTC	GCC	GGC	GAC	GCA	TGG	CGC	ACC	AAC	CTC	CCA	TAT	CGC	TTC	594
His	Asp	Arg	Arg	Phe	Ala	Gly	Asp	Ala	Trp	Arg	Thr	Asn	Leu	Pro	Tyr	Arg	Phe	
				185					190					195				
GCT	GCC	GCG	TTC	TAC	CTG	CTC	AAT	GCG	CGC	GCC	TTG	ACC	GAG	CTG	GCC	GAT	GCC	648
Ala	Ala	Ala	Phe	Tyr	Leu	Leu	Asn	Ala	Arg	Ala	Leu	Thr	Glu	Leu	Ala	Asp	Ala	
	200				205						210				215			
GTC	GAG	GCC	GAT	GCC	AAG	ACC	CGC	CAG	CGC	ATC	CGC	TTC	GCG	ATC	TCG	CAA	TGG	702
Val	Glu	Ala	Asp	Ala	Lys	Thr	Arg	Gln	Arg	Ile	Arg	Phe	Ala	Ile	Ser	Gln	Trp	
			220				225						230					
GTC	GAT	GCG	ATG	TCG	CCC	GCC	AAC	TTC	CTT	GCC	ACC	AAT	CCC	GAG	GCG	CAG	CGC	756
Val	Asp	Ala	Met	Ser	Pro	Ala	Asn	Phe	Leu	Ala	Thr	Asn	Pro	Glu	Ala	Gln	Arg	
	235				240					245					250			
CTG	CTG	ATC	GAG	TCG	GGC	GGC	GAA	TCG	CTG	CGT	GCC	GGC	GTG	CGC	AAC	ATG	ATG	810
Leu	Leu	Ile	Glu	Ser	Gly	Gly	Glu	Ser	Leu	Arg	Ala	Gly	Val	Arg	Asn	Met	Met	
		255				260						265				270		
GAA	GAC	CTG	ACA	CGC	GGC	AAG	ATC	TCG	CAG	ACC	GAC	GAG	AGC	GCG	TTT	GAG	GTC	864
Glu	Asp	Leu	Thr	Arg	Gly	Lys	Ile	Ser	Gln	Thr	Asp	Glu	Ser	Ala	Phe	Glu	Val	
				275					280					285				
GGC	CGC	AAT	GTC	GCG	GTG	ACC	GAA	GGC	GCC	GTG	GTC	TTC	GAG	AAC	GAG	TAC	TTC	918
Gly	Arg	Asn	Val	Ala	Val	Thr	Glu	Gly	Ala	Val	Val	Phe	Glu	Asn	Glu	Tyr	Phe	
	290					295						300				305		



CAG Gln	CTG Leu	TTG Leu	CAG Gln 310	TAC Tyr	AAG Lys	CCG Pro	CTG Leu	ACC Thr 315	GAC Asp	AAG Lys	GTG Val	CAC His	GCG Ala 320	CGC Arg	CCG Pro	CTG Leu	CTG Leu	972
ATG Met 325	GTG Val	CCG Pro	CCG Pro	TGC Cys	ATC Ile 330	AAC Asn	AAG Lys	TAC Tyr	TAC Tyr	ATC Ile 335	CTG Leu	GAC Asp	CTG Leu	CAG Gln	CCG Pro	GAG Glu	AGC Ser	1026
TCG Ser	CTG Leu	GTG Val 345	CGC Arg	CAT His	GTG Val	GTG Val	GAG Glu 350	CAG Gln	GGA Gly	CAT His	ACG Thr	GTG Val 355	TTT Phe	CTG Leu	GTG Val	TCG Ser	TGG Trp 360	1080
CGC Arg	AAT Asn	CCG Pro	GAC Asp	GCC Ala 365	AGC Ser	ATG Met	GCC Ala	GGC Gly	AGC Ser 370	ACC Thr	TGG Trp	GAC Asp	GAC Asp	TAC Tyr 375	ATC Ile	GAG Glu	CAC His	1134
GCG Ala 380	GCC Ala	ATC Ile	CGC Arg	GCC Ala	ATC Ile	GAA Glu 385	GTC Val	GCG Ala	CGC Arg	GAC Asp	ATC Ile 390	AGC Ser	GGC Gly	CAG Gln	GAC Asp	AAG Lys 395	ATC Ile	1188
AAC Asn	GTG Val	CTC Leu	GGC Gly 400	TTC Phe	TGC Cys	GTG Val	GGC Gly 405	GGC Gly	ACC Thr	ATT Ile	GTC Val	TCG Ser	ACC Thr 410	GCG Ala	CTG Leu	GCG Ala	GTG Val	1242
CTG Leu 415	GCC Ala	GCG Ala	CGC Arg	GGC Gly	GAG Glu 420	CAC His	CCG Pro	GCC Ala	GCC Ala	AGC Ser 425	GTC Val	ACG Thr	CTG Leu	CTG Leu	ACC Thr 430	ACG Thr	CTG Leu	1296
CTG Leu	GAC Asp	TTT Phe 435	GCC Ala	GAC Asp	ACG Thr	GGC Gly 440	ATC Ile	CTC Leu	GAC Asp	GTC Val	TTT Phe 445	GTC Val	GAC Asp	GAG Glu	GGC Gly	CAT His	GTG Val 450	1350
CAG Gln	TTG Leu	CGC Arg	GAG Glu 455	GCC Ala	ACG Thr	CTG Leu	GGC Gly	GGC Gly	GGC Gly 460	GCC Ala	GGC Gly	GCG Ala	CCG Pro	TGC Cys 465	GCG Ala	CTG Leu	CTG Leu	1404
CGC Arg 470	GGC Gly	CTT Leu	GAG Glu	CTG Leu	GCC Ala	AAT Asn 475	ACC Thr	TTC Phe	TCG Ser	TTC Phe	TTG Leu 480	CGC Arg	CCG Pro	AAC Asn	GAC Asp 485	CTG Leu	GTG Val	1458
TGG Trp	AAC Asn	TAC Tyr	GTG Val 490	GTC Val	GAC Asp	AAC Asn	TAC Tyr	CTG Leu 495	AAG Lys	GGC Gly	AAC Asn	ACG Thr	CCG Pro	GTG Val	CCG Pro	TTC Phe	GAC Asp	1512
CTG Leu 505	CTG Leu	TTC Phe	TGG Trp	AAC Asn	GGC Gly 510	GAC Asp	GCC Ala	ACC Thr	AAC Asn	CTG Leu 515	CCG Pro	GGG Gly	CCG Pro	TGG Trp	TAC Tyr 520	TGC Cys	TGG Trp	1566
TAC Tyr	CTG Leu	CGC Arg	CAC His	ACC Thr	TAC Tyr	CTG Leu	CAG Gln 530	AAC Asn	GAG Glu	CTC Leu	AAG Lys	GTA Val 535	CCG Pro	GGC Gly	AAG Lys	CTG Leu	ACC Thr 540	1620
GTG Val	TGC Cys	GGC Gly	GTG Val	CCG Pro	GTG Val	GAC Asp	CTG Leu	GCC Ala	AGC Ser 550	ATC Ile	GAC Asp	GTG Val	CCG Pro	ACC Thr 555	TAT Tyr	ATC Ile	TAC Tyr	1674
GGC Gly 560	TCG Ser	CGC Arg	GAA Glu	GAC Asp	CAT His	ATC Ile 565	GTG Val	CCG Pro	TGG Trp	ACC Thr	GCG Ala 570	GCC Ala	TAT Tyr	GCC Ala	TCG Ser	ACC Thr 575	GCG Ala	1728
CTG Leu	CTG Leu	GCG Ala	AAC Asn 580	AAG Lys	CTG Leu	CGC Arg	TTC Phe	GTG Val 585	CTG Leu	GGT Gly	GCG Ala	TCG Ser	GGC Gly 590	CAT His	ATC Ile	GCC Ala	GGT Gly	1782
GTG Val 595	ATC Ile	AAC Asn	CCG Pro	CCG Pro	GCC Ala 600	AAG Lys	AAC Asn	AAG Lys	CGC Arg	AGC Ser 605	CAC His	TGG Trp	ACT Thr	AAC Asn	GAT Asp 610	GCG Ala	CTG Leu	1836

CCG	GAG	TCG	CCG	CAG	CAA	TGG	CTG	GCC	GGC	GCC	ATC	GAG	CAT	CAC	GGC	AGC	TGG	1890
Pro	Glu	Ser 615	Pro	Gln	Gln	Trp	Leu 620	Ala	Gly	Ala	Ile	Glu 625	His	His	Gly	Ser	Trp 630	
TGG	CCG	GAC	TGG	ACC	GCA	TGG	CTG	GCC	GGG	CAG	GCC	GGC	GCG	AAA	CGC	GCC	GCG	1944
Trp	Pro	Asp	Trp	Thr 635	Ala	Trp	Leu	Ala	Gly 640	Gln	Ala	Gly	Ala	Lys 645	Arg	Ala	Ala	
CCC	GCC	AAC	TAT	GGC	AAT	GCG	CGC	TAT	CGC	GCA	ATC	GAA	CCC	GCG	CCT	GGG	CGA	1998
Pro	Ala 650	Asn	Tyr	Gly	Asn	Ala 655	Arg	Tyr	Arg	Ala	Ile 660	Glu	Pro	Ala	Pro	Gly 665	Arg	
TAC	GTC	AAA	GCC	AAG	GCA	TGA												2019
Tyr	Val	Lys	Ala 670	Lys	Ala	***												

**WHAT IS CLAIMED IS:**

1. A transgenic plant material having plastids, the plant material characterized in that it contains foreign DNA encoding a bacterial polypeptide which is selected from the group consisting of 3 ketothiolase, acetoacetyl-CoA reductase and polyhydroxyalkanoate (PHA) synthase and mixtures thereof leading to the production of a polyhydroxyalkanoate in the plastid in the plant.
2. The plant material of Claim 1 wherein the polyhydroxyalkanoate (PHA) is polyhydroxybutyrate (PHB) and wherein coding sequence of the DNA and RNA for the production of the enzymes leading to polyhydroxybutyrate (PHB) synthesis are as shown in SEQ. ID NO: 1, SEQ. ID NO: 2 and SEQ. ID NO: 3.
3. A transgenic plant material having plastids, the plant material characterized in that it contains foreign DNA encoding a peptide which exhibits 3-ketothiolase activity in the plastid in the plant.
4. The plant material of Claim 3 wherein the DNA which contains an open reading frame is shown in SEQ. ID NO: 1.
5. A transgenic plant material having plastids, the plant material characterized in that it contains foreign DNA encoding acetoacetyl-CoA reductase activity in the plastid of the plant.
6. The transgenic plant material of Claim 5 wherein the DNA which contains an open reading frame is shown in SEQ. ID NO: 2.
7. A transgenic plant material having plastids, the plant material characterized in that it contains foreign DNA encoding a polypeptide which exhibits PHA synthase activity in the plastid of the plant.
8. The plant material of Claim 7 wherein the DNA is in SEQ. ID NO: 3.
9. The plant material of any one of Claims 1-8 as an embryo, seed or propagule of the seed.

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10. A method for introducing foreign DNA encoding polypeptides leading to the synthesis of a polyhydroxyalkanoate (PHA) in a plastid in a plant which comprises mating by sexual fertilization two plants which do not produce PHA, each containing foreign DNA from a bacterium encoding one or more different enzymes in a pathway leading to polymerization of hydroxyacyl-CoA by PHA synthase to produce the plant which synthesizes the PHA in a plastid in the plant.
11. The method of Claim 10 wherein PHA is polyhydroxybutyrate (PHB).
12. A gene segment as contained in plastid pBI-TPSS-Thio or pBIB-CCN Thio encoding a modified 3-ketothiolase gene for targeting to a plastid of a plant.
13. A gene segment as contained in plastid pBI-TPSS-Red from *Alcaligenes eutrophus* encoding a modified acetoacetyl-CoA reductase gene for targeting to plastid of a plant.
14. A gene segment as contained in plasmid pBI-TPSS-Syn or pBIB-HCN Syn from *Alcaligenes eutrophus* encoding a modified polyhydroxybutyrate (PHB) synthase gene for targeting to a plastid of a plant.
15. A plant containing the gene segment of any one of Claims 12-14.
16. The polyhydroxyalkanoate produced by the plant material of any one of Claims 1-9.

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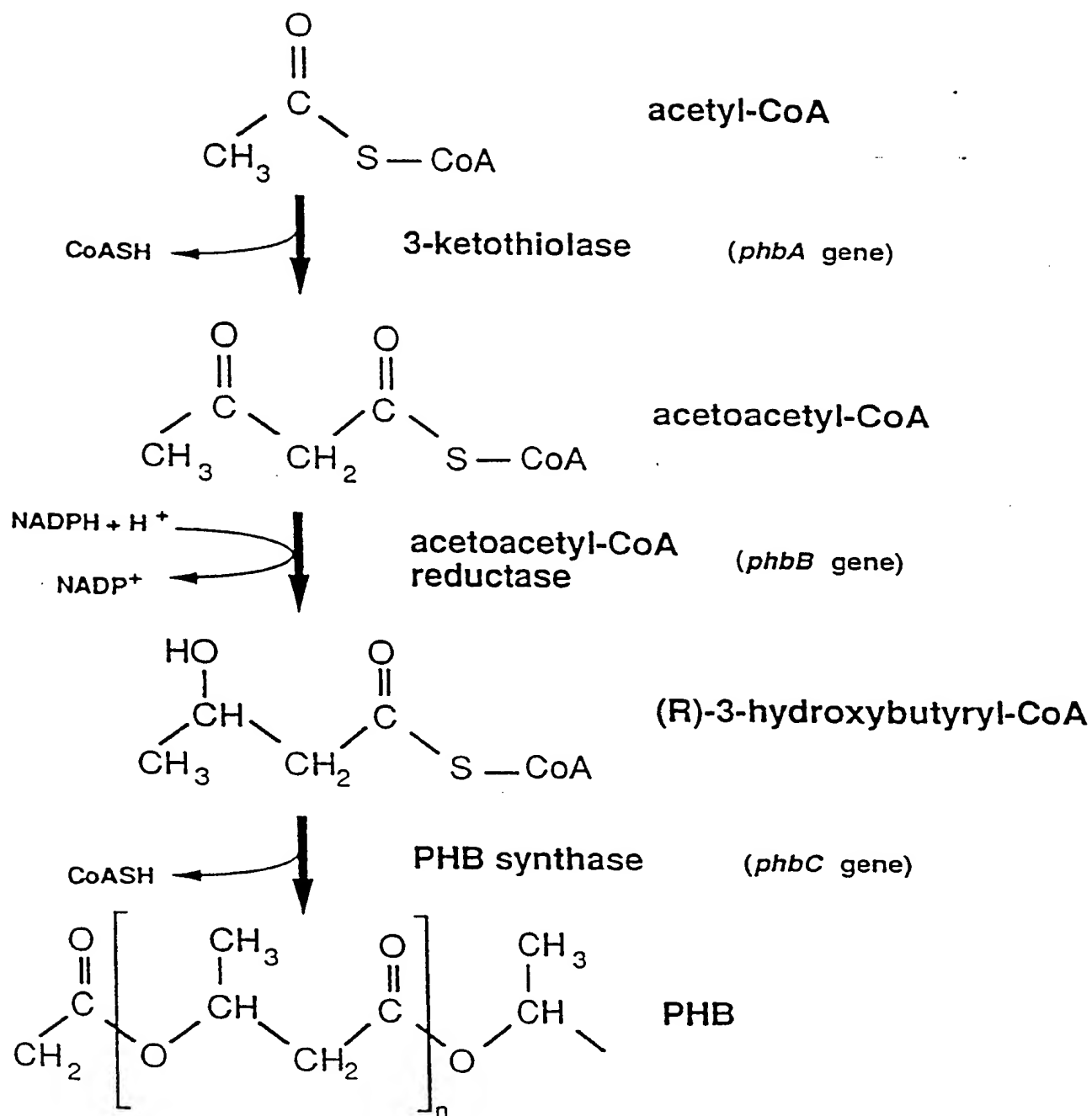


FIG. 1

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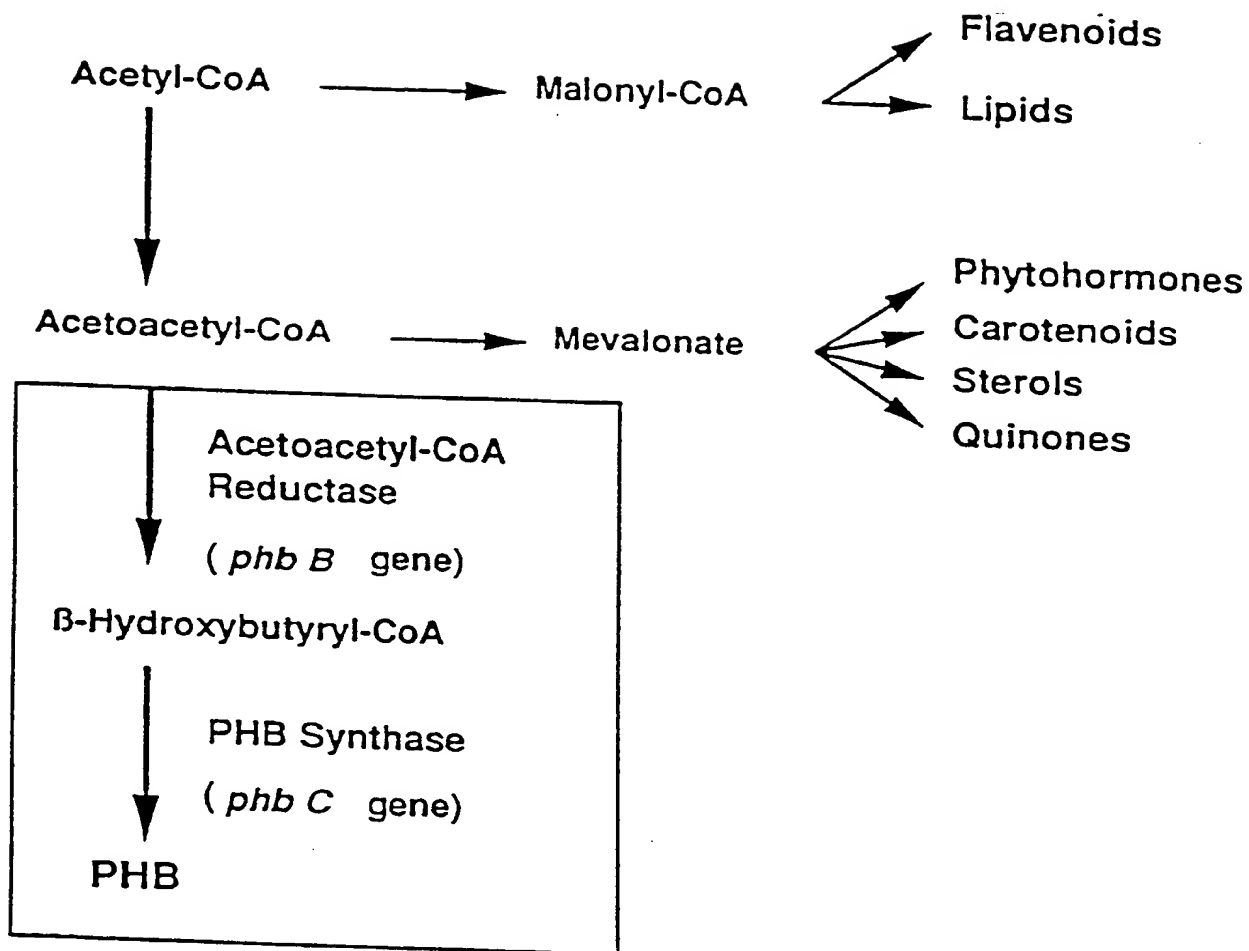


FIG. 2

FIG. 3a

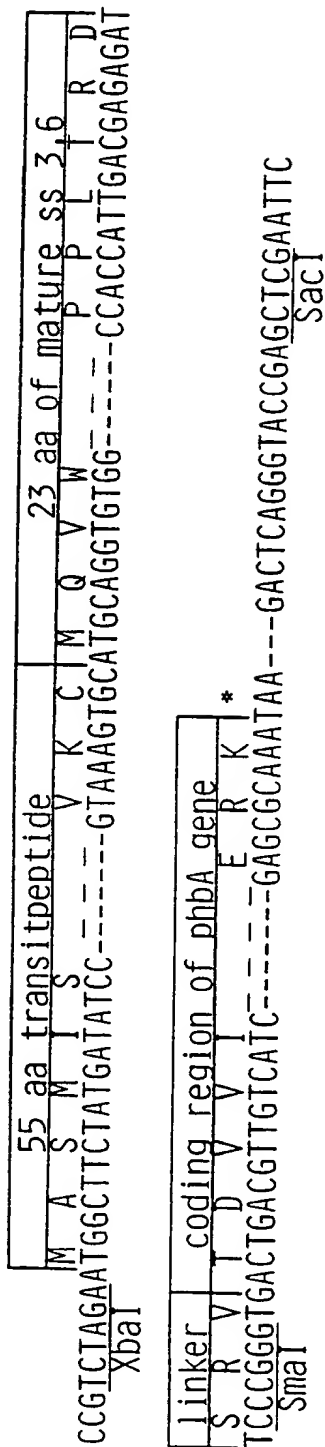


FIG. 3b

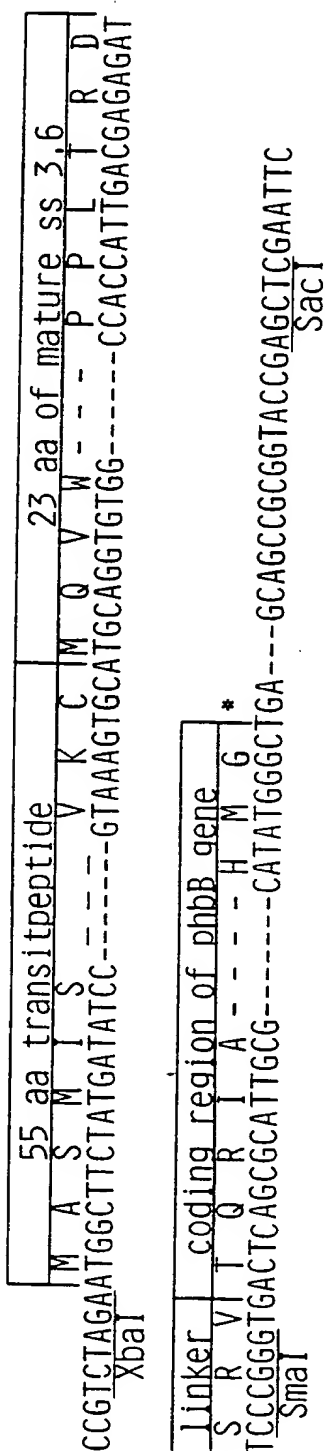


FIG. 3c

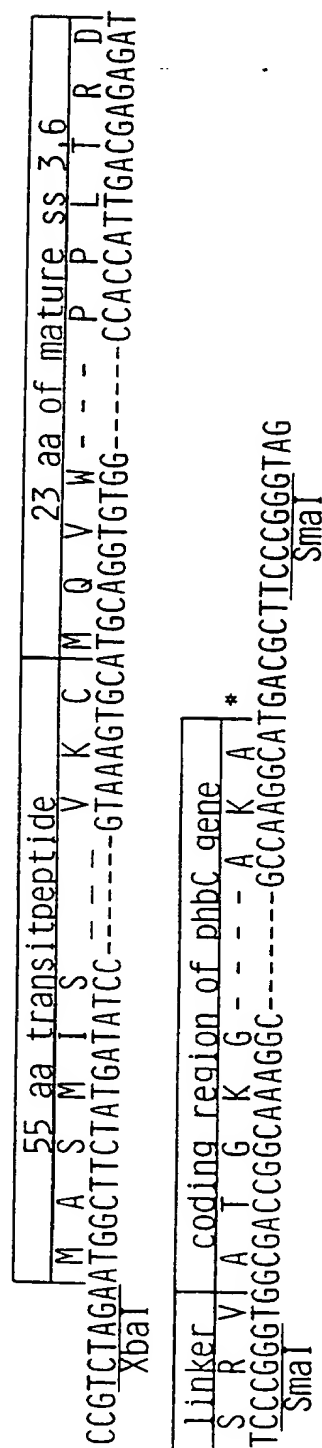


FIG. 4A

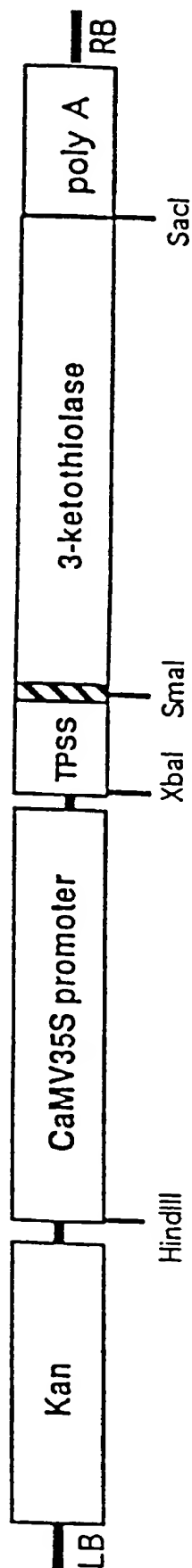


FIG. 4B

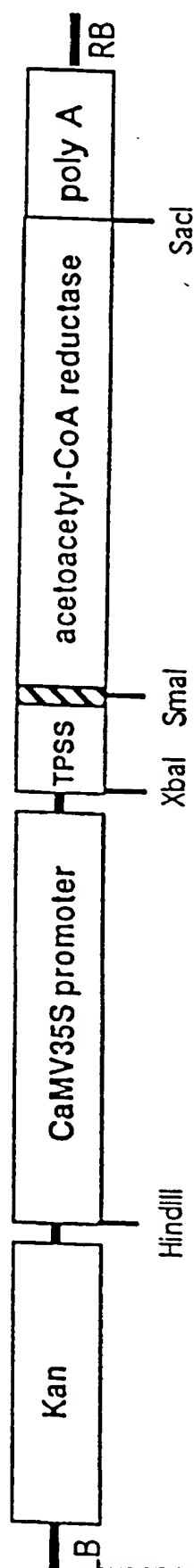
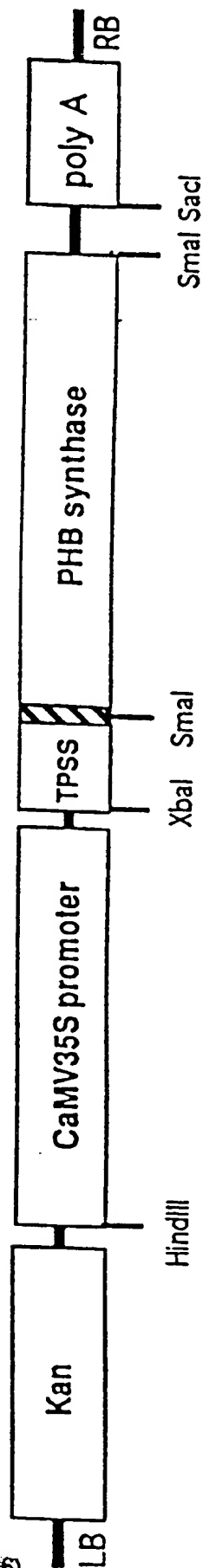


FIG. 4C





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FIG. 5A

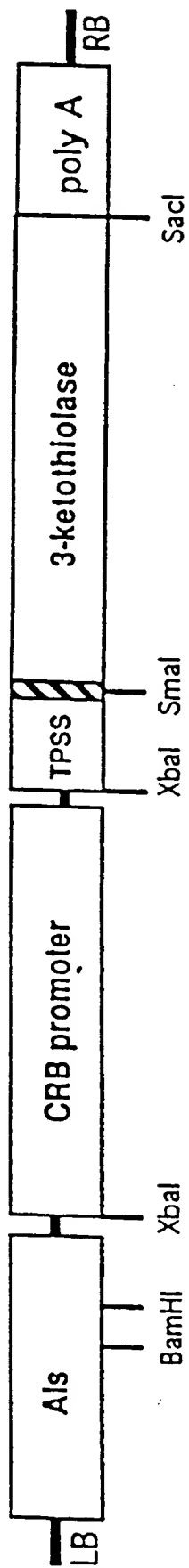


FIG. 5B

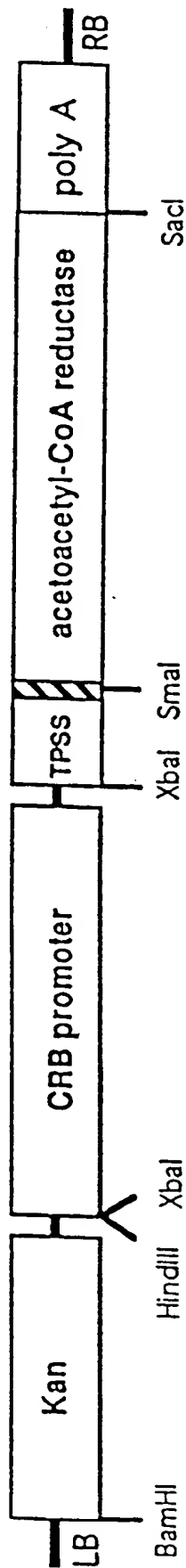
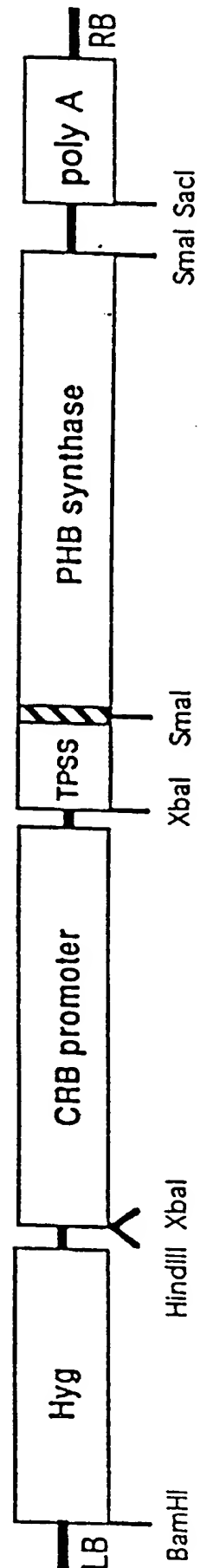


FIG. 5C



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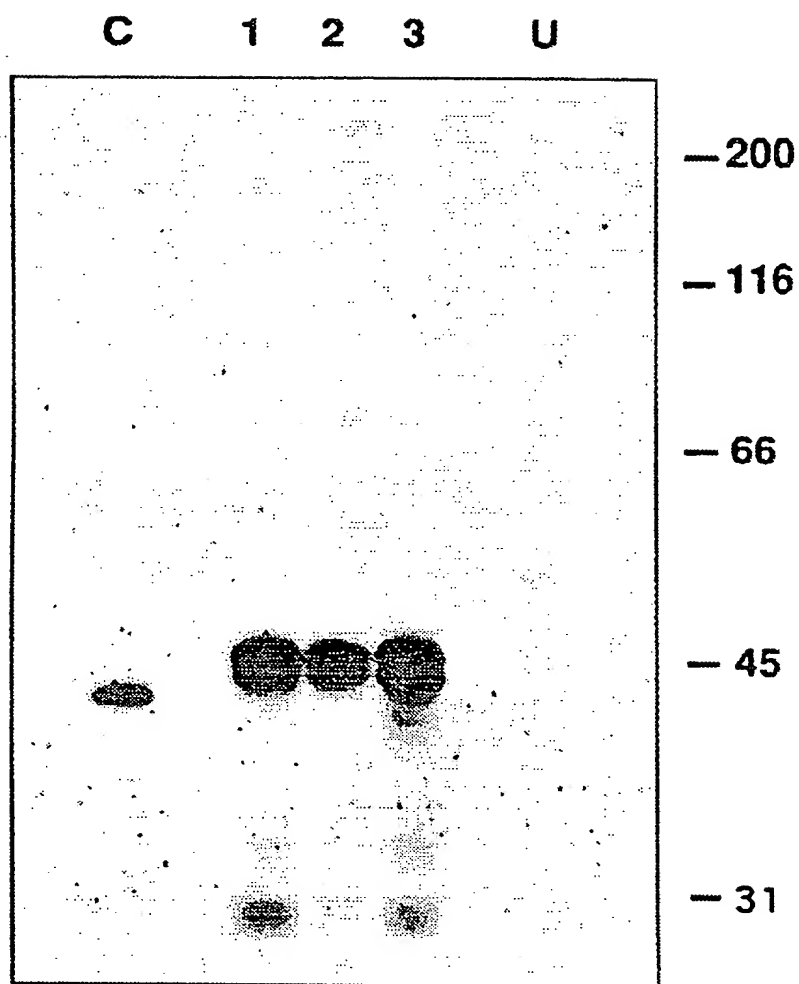


FIG. 6

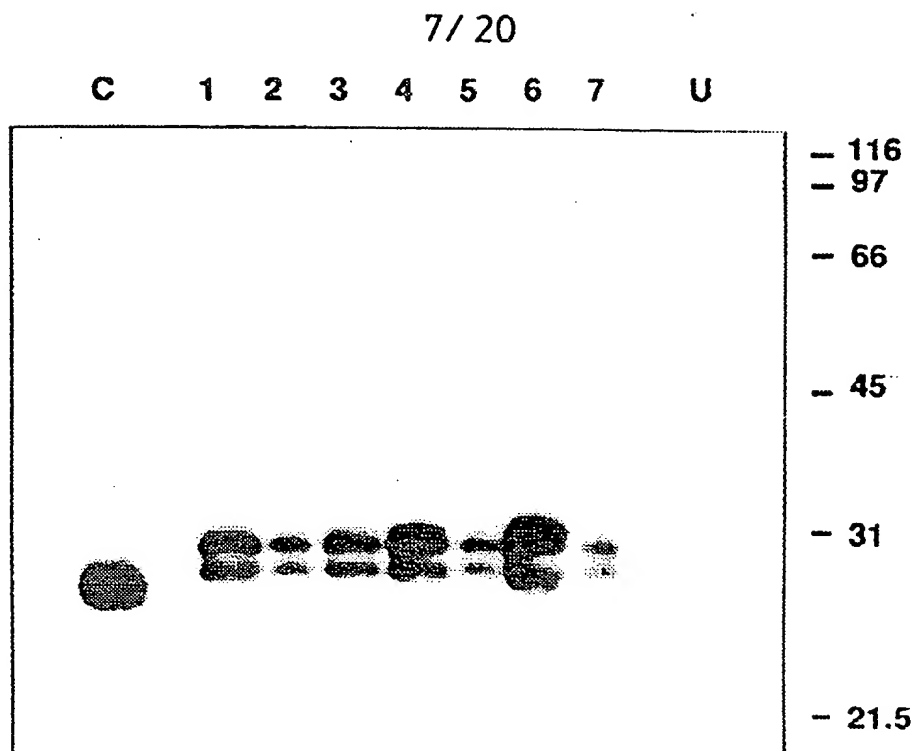


FIG. 7

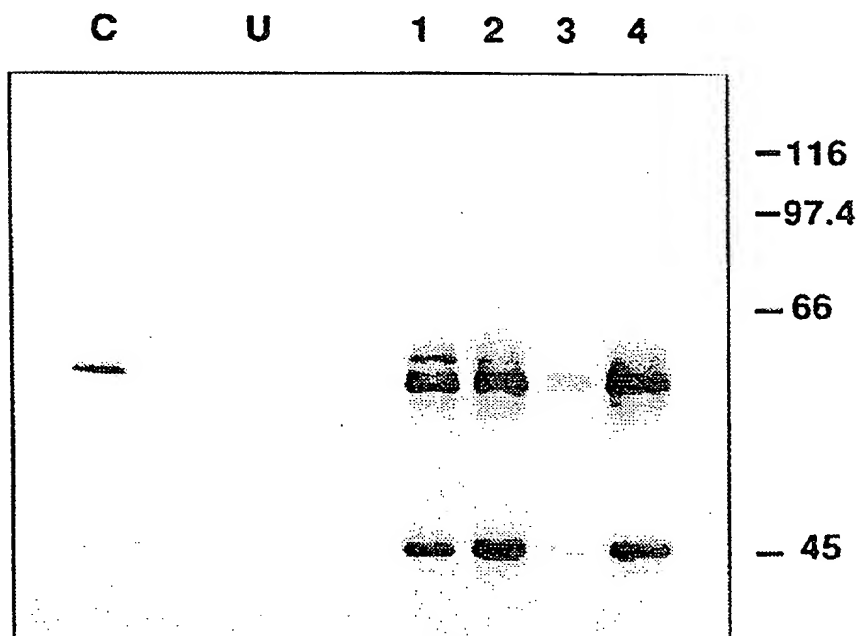
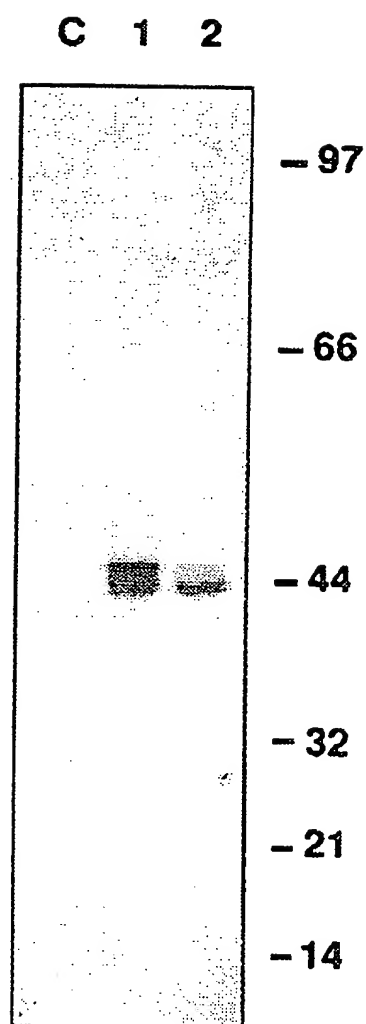


FIG. 8

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**FIG. 9**

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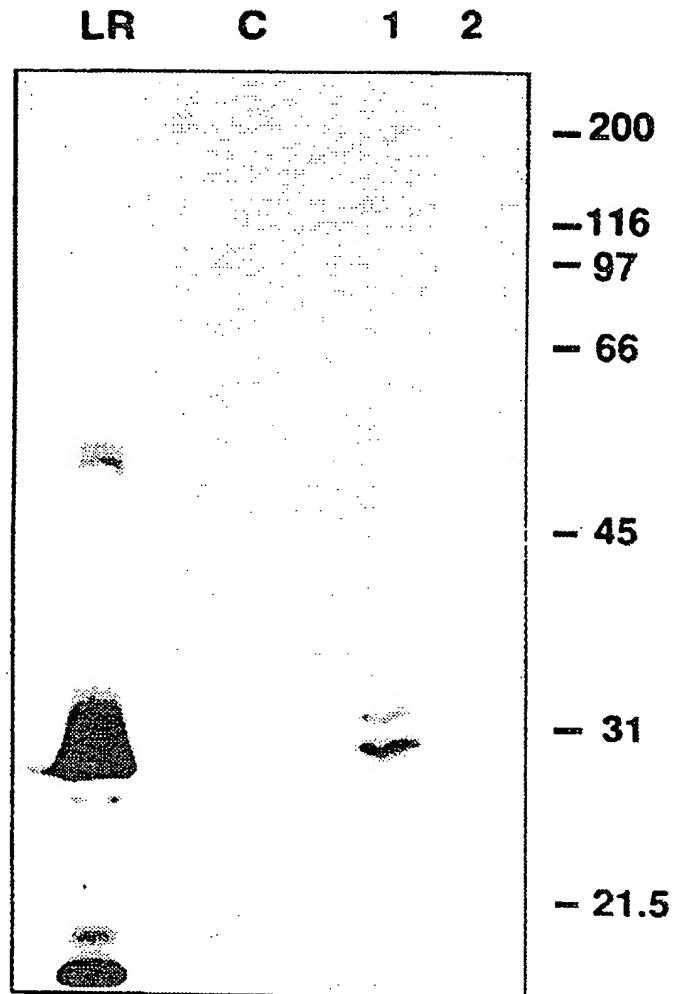


FIG. 10

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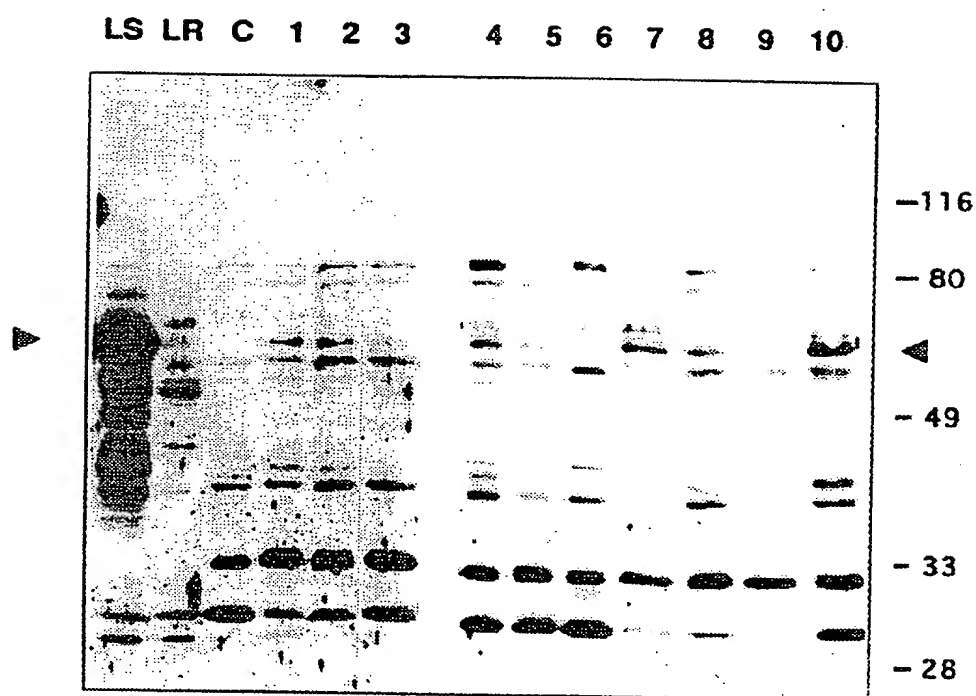


FIG. II

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FIG. 12a

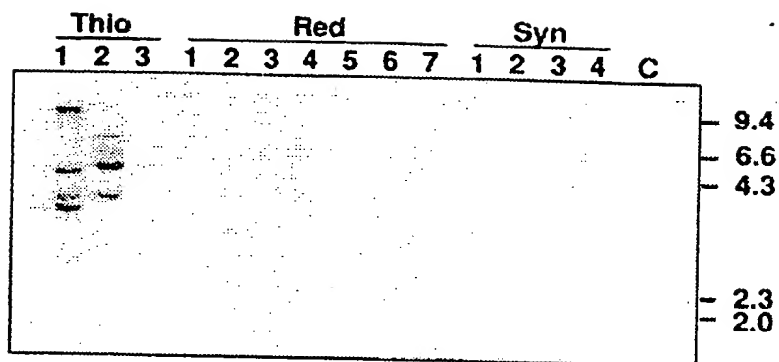


FIG. 12b

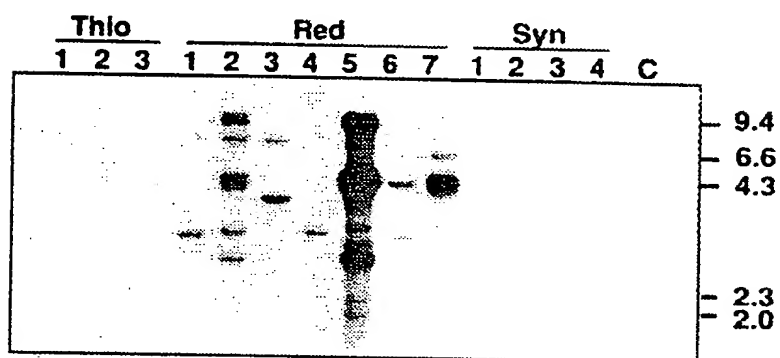
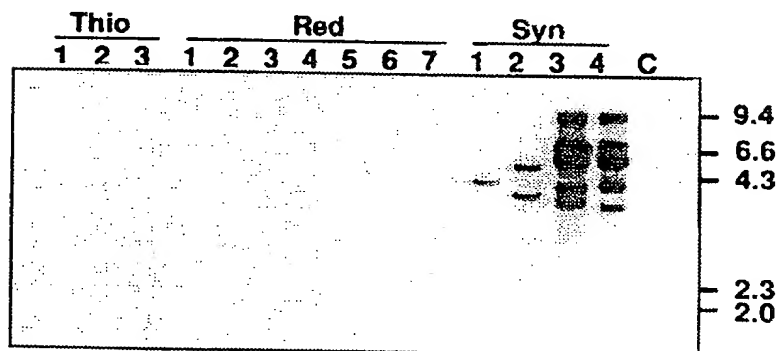


FIG. 12c



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FIG. 13a

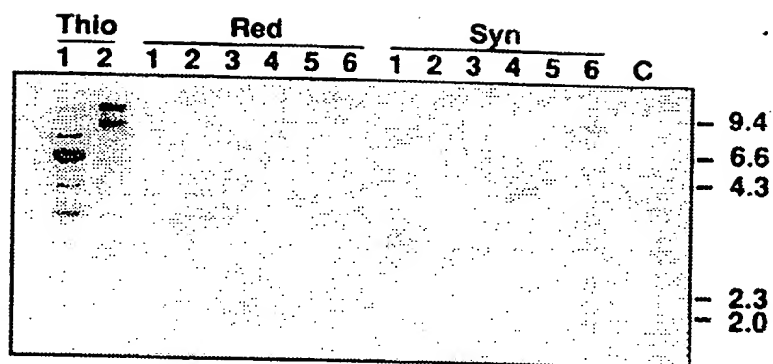


FIG. 13b

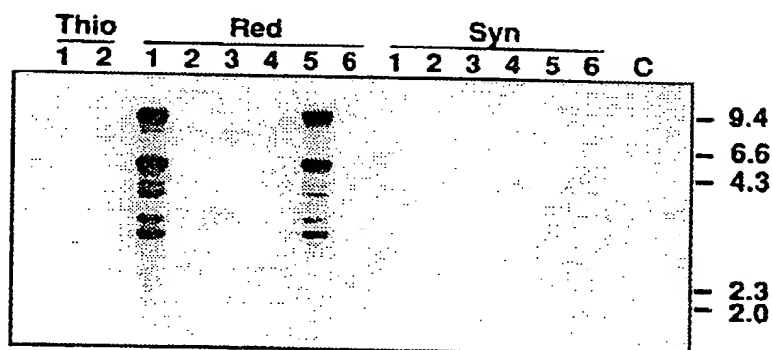
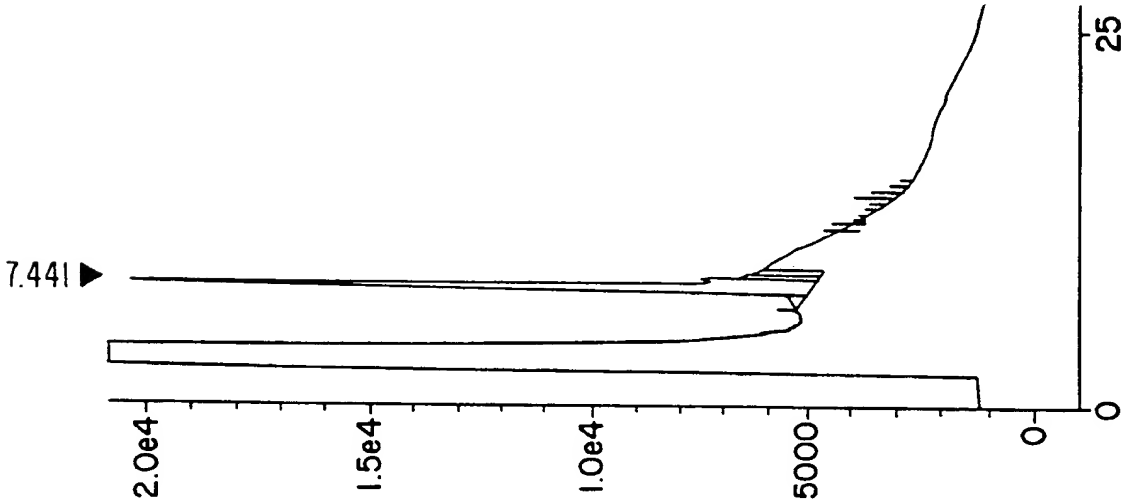
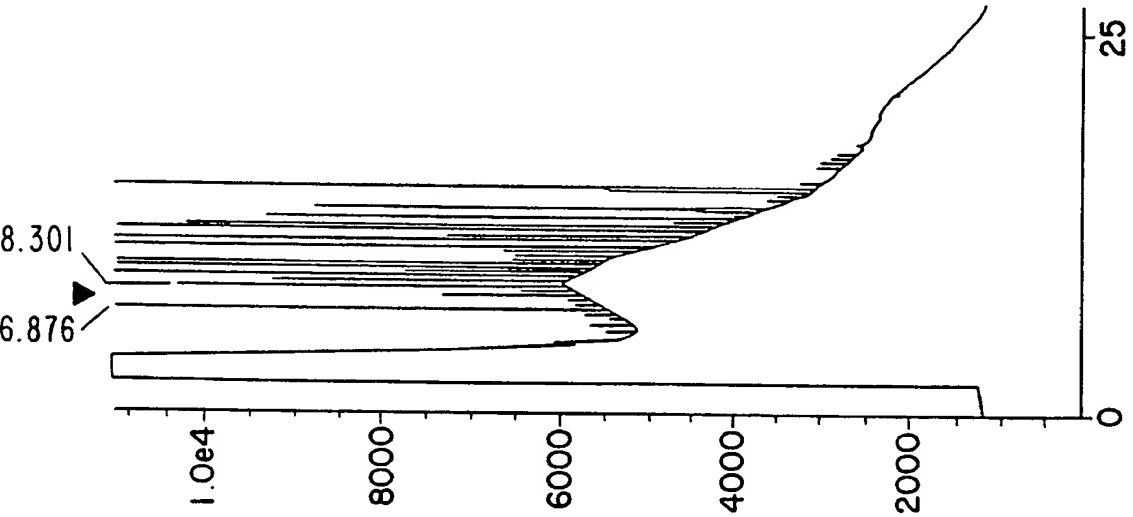
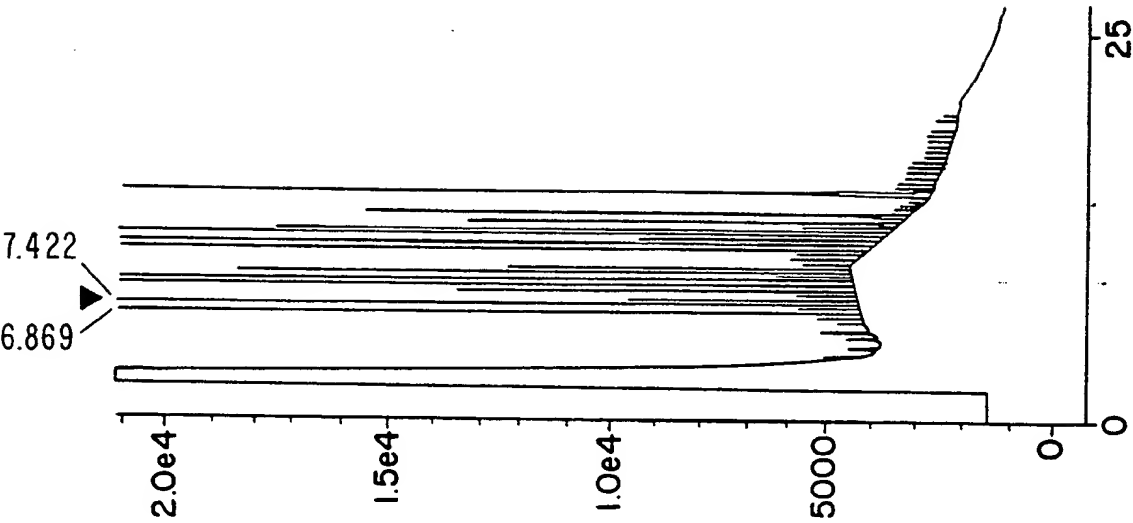


FIG. 13c







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RELATIVE ABUNDANCE

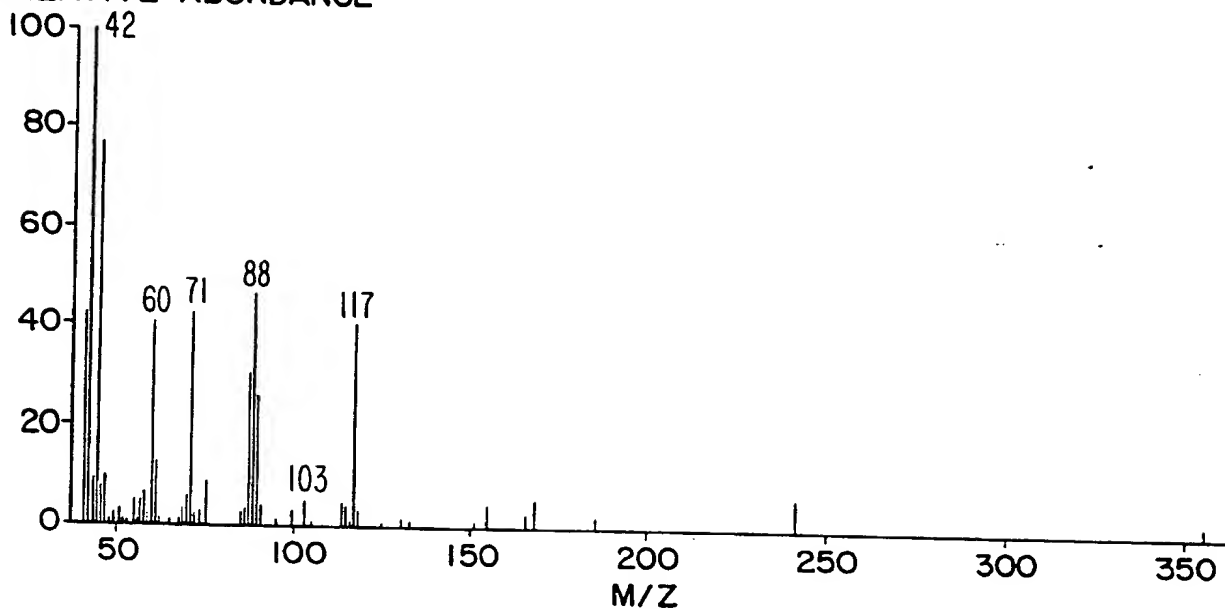


FIG. 15A

RELATIVE ABUNDANCE

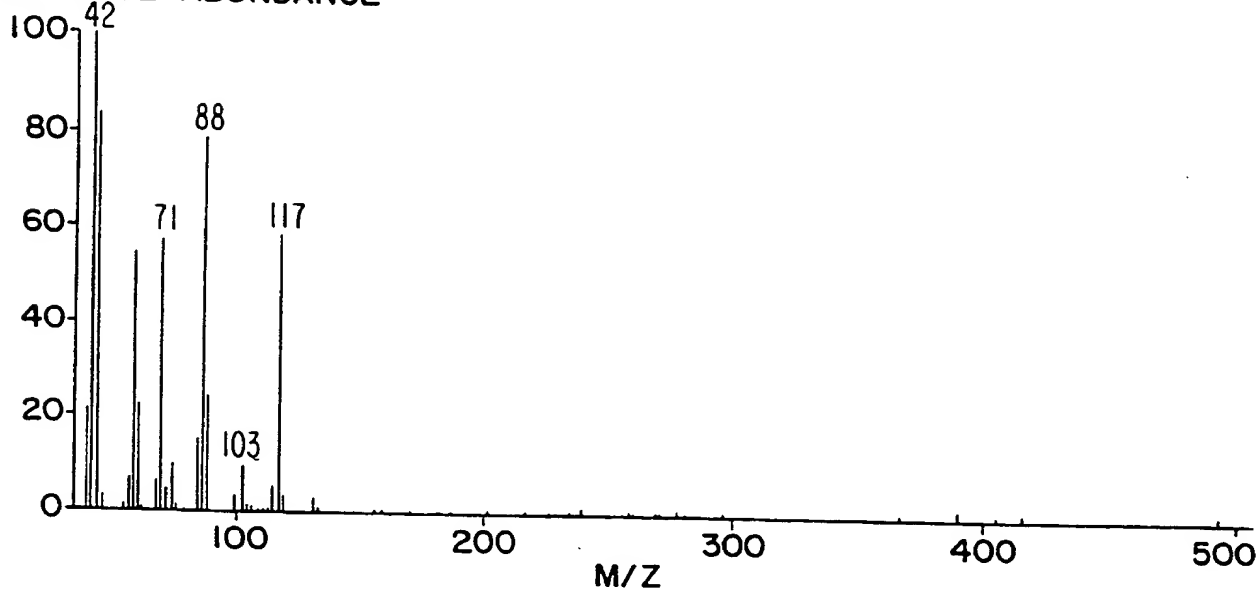
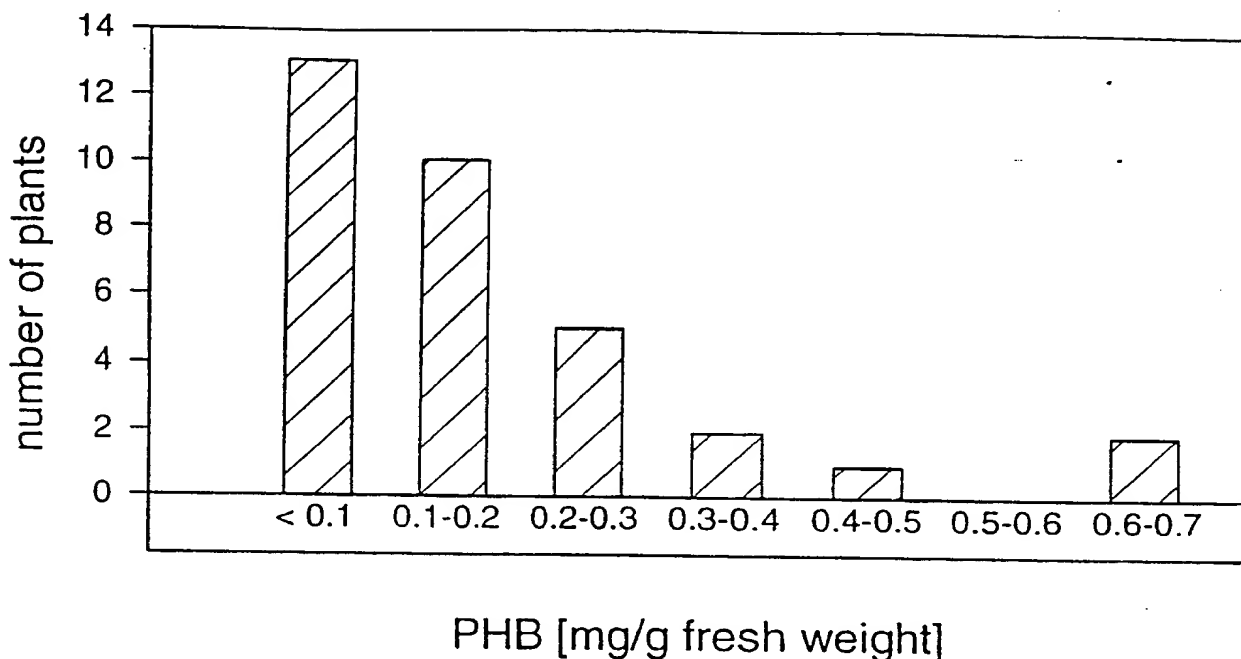
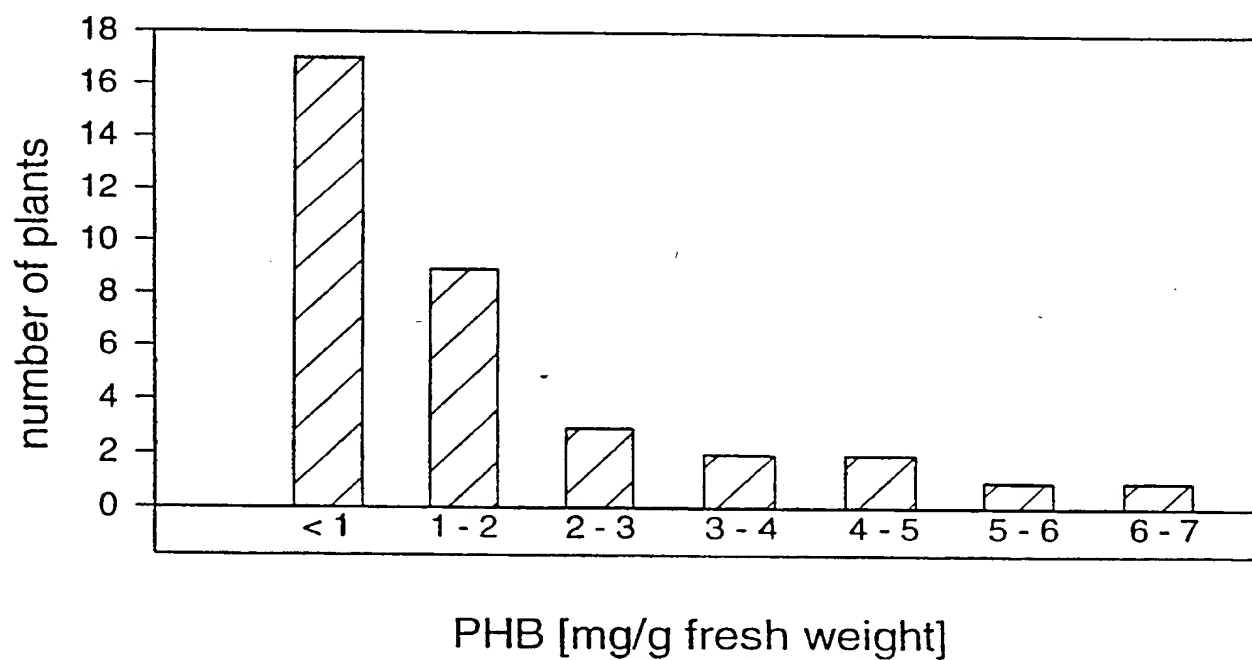


FIG. 15B

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**FIG.16A****FIG.16B**

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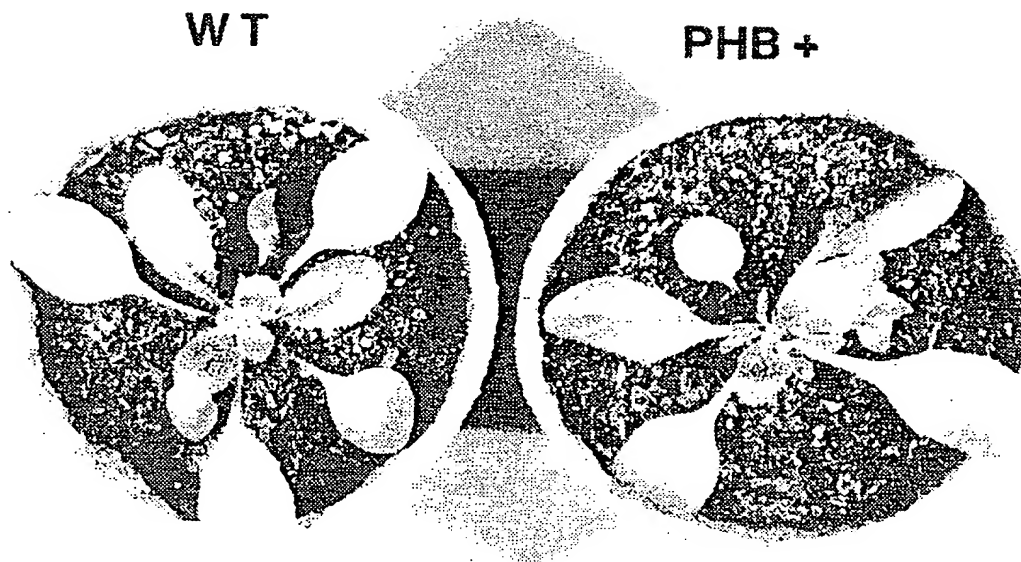


FIG.17A

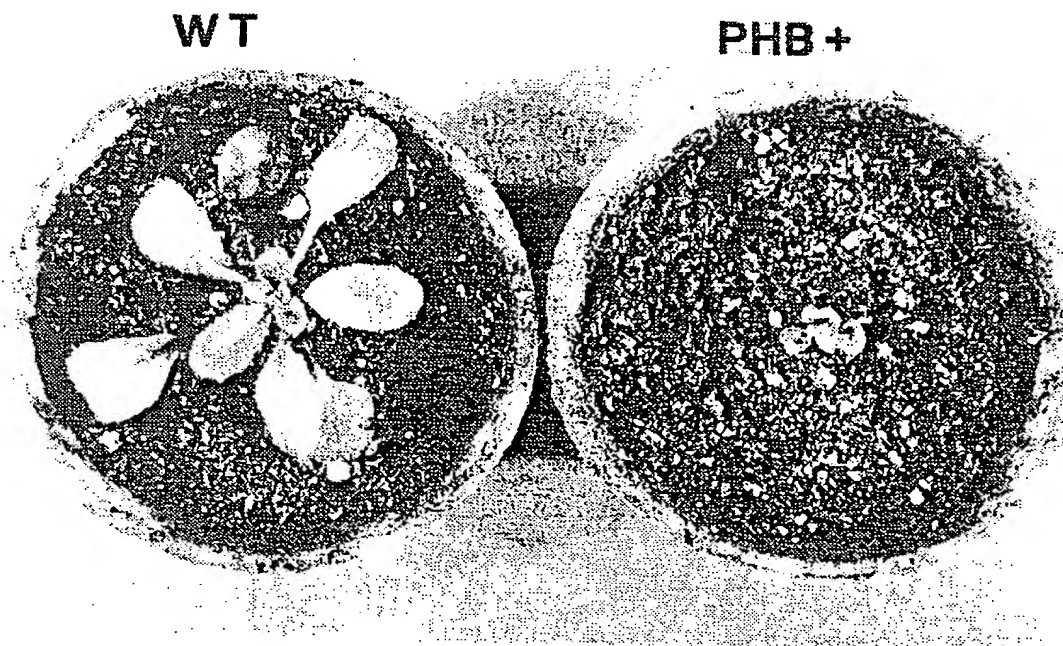


FIG.17B

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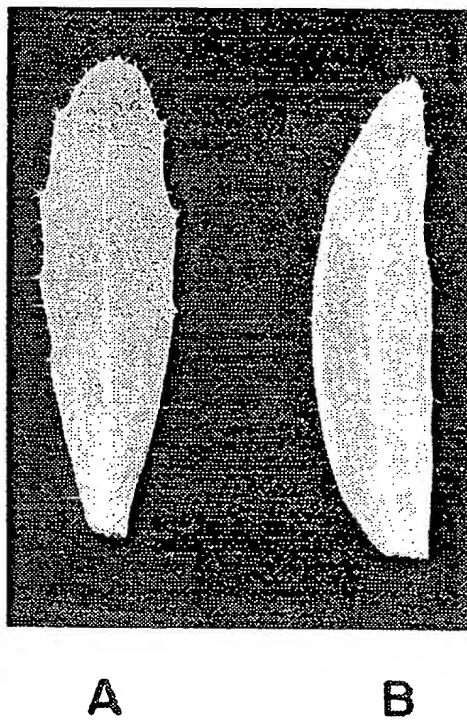


FIG.18

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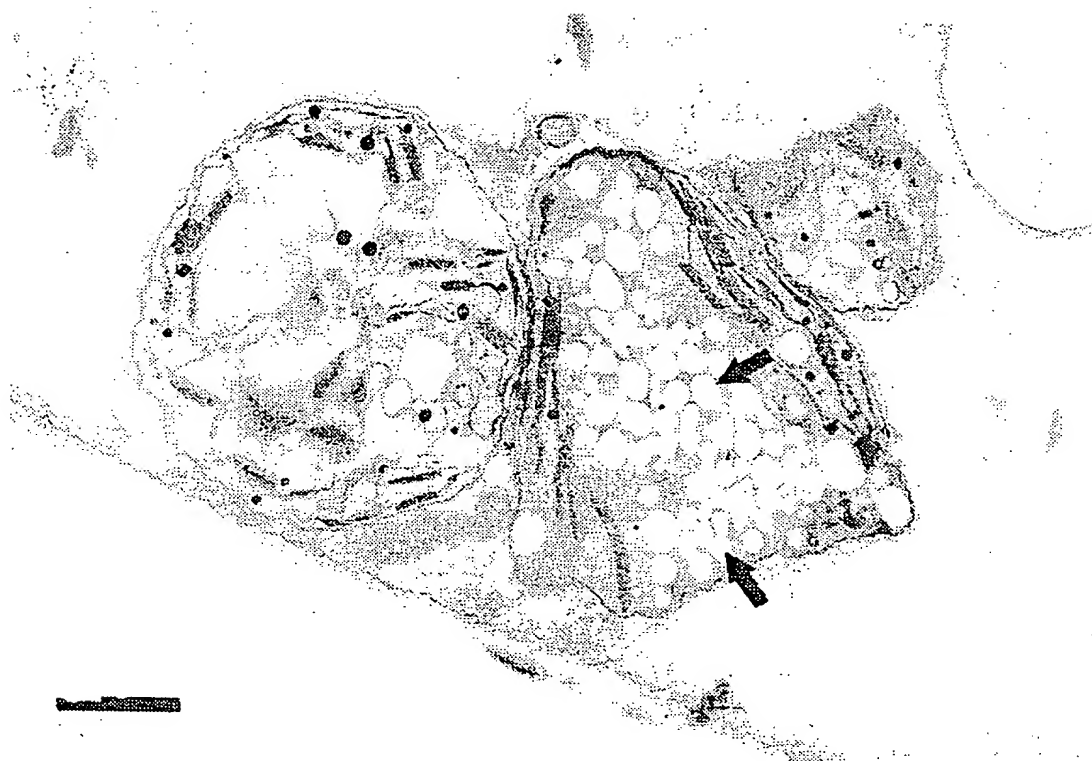


FIG. 19A

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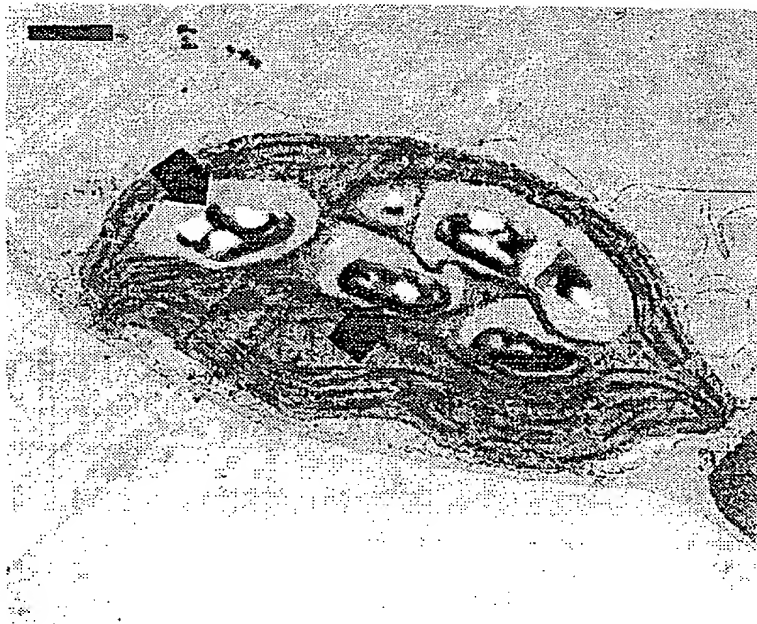


FIG. 19B

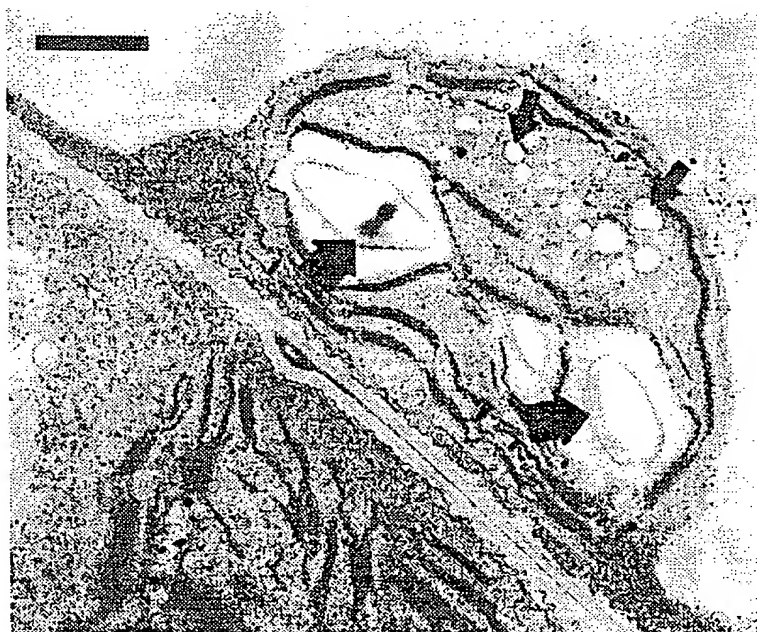


FIG. 19C

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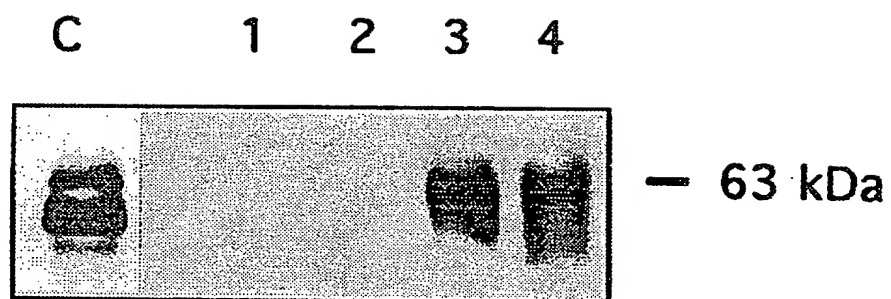


FIG. 20